

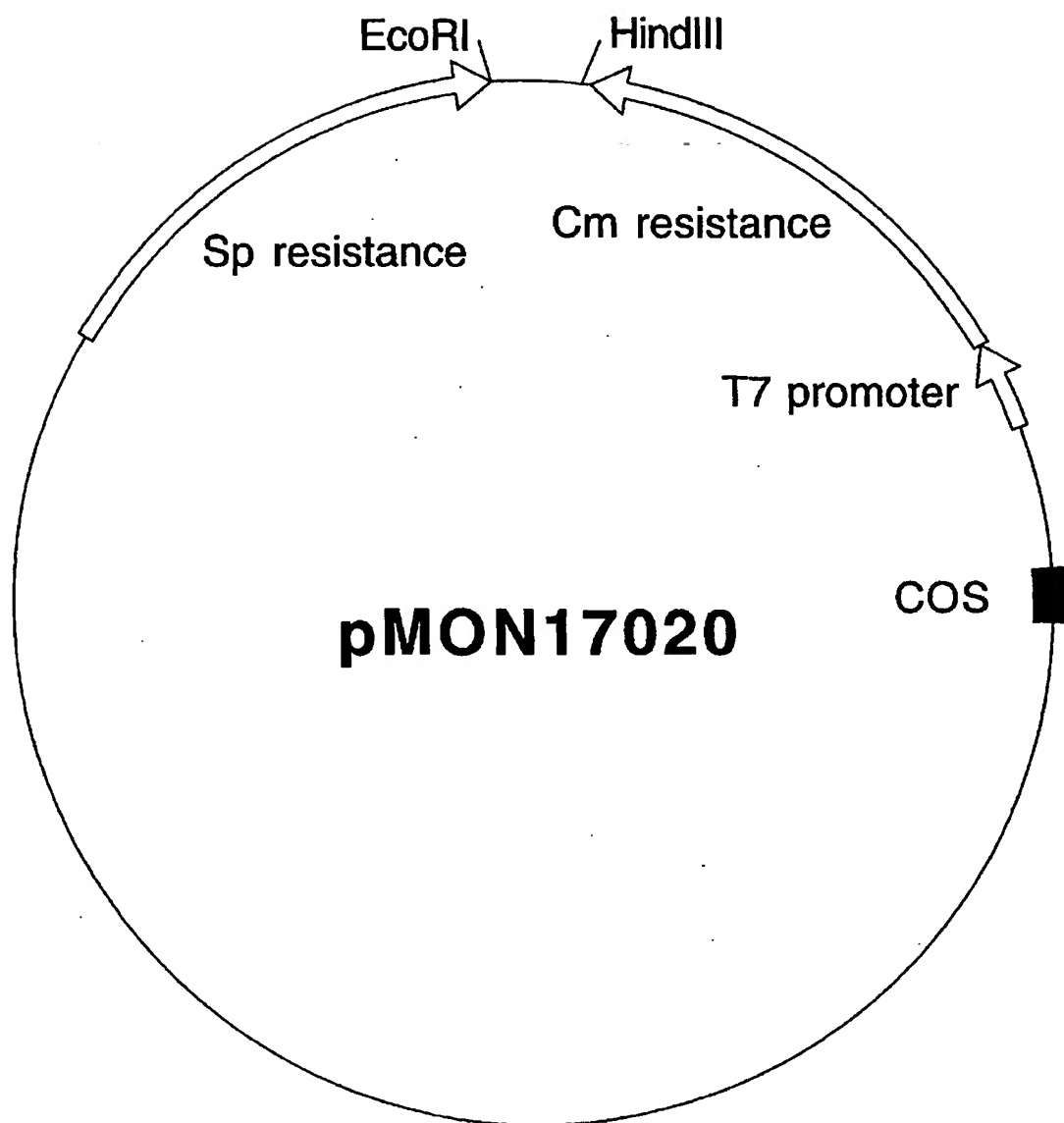
SSPI
TCATCAAAATATTTAGCAGCATTCAGATTGGGTTCAATCAACAAGGTACGAGCCATATC 6417
6358 AGTAGTTTATAAATCGTCGTAAGGTCTAACCCTAAGTTAGTTGTTCCATGCTCGGTATAG
ACTTTATTCAAATTTGGTATCGCCAAAAACCAAGAAGAACTCCCATCCTCAAAAGGTTTGTGTA 6477
6418 TGAAATAAGTTTAACCATAGCGGTTTGTGTTCTTCCCTTGAGGTAGGAGTTTCCAAACAT
AGGAAGAATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTA 6537
6478 TCCTTCTTAAGAGTCAGGTTTCGGAGTTGTGTTCCAGTCCCATGTCTCAGAGGTTTGGTAAT
GCCAAAAGCTACAGGAGATCAATGAAGAAATCTTCAATCAAAAGTAAACTACTGTTCAGCA 6597
6538 CGGTTTTTCGATGTCCCTCTAGTTACTTCTTAGAAGTTAGTTTTCATTTTGATGACAAAGTTCGT
CATGCATCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGG 6657
6598 GTACGTAGTACCAGTCATTCAAAGTCTTTTCTGTAGGTGGCTTCTGAATTTTCAATCACC

Figure 1A

GCATCTTTGAAAGTAAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACGACAAAAA 6717
6658 CGTAGAAACTTTTCATTAGAACAGTTGTAGCTCGTCGACCGAACACCCCTGGTCTGTTT
AGGAATGGTGCAGAAATTGTTAGGCGCACCTACCAAAGCATCTTTGCCCTTTATTGCAAG 6777
6718 TCCTTACCACGCTTTAAACAAATCCCGGTGGATGGTTTTCGTAGAAACGGAAATAACGTTTC
ATAAAGCAGATTCCCTCTAGTACAAGTGGGGAACAAAAATAACGTGGAAGAGCTGTCTCTG 6837
6778 TATTTCTAAGGAGATCATGTTCAACCCCTTGTTTATTGTCACCTTTTCTCGACAGGAC
ACAGCCCACTCACTAATGCGTATGACGAACGCAGTGACGACCAACAAAGAAATTCCTCTTA 6897
6838 TGTCCGGTGAGTGATTACGCATACTGCTTGCGTCACCTGCTGGTGTTCCTTAAGGGAGAT
TATAAGAAGGCATTCAATCCCATTTGAAGGATCATCAGATACTAACCAATATTTCTC
6898 ATATTCTCCCGTAAGTAAGGGTAAACTTCCTAGTAGTCTATGATTGGTTATAAAGAG 6954

SspI

Figure 1B

**Figure 2**

```

AAGCCCCGCGT TCTCTCCGGC GCTCCGCCCG GAGAGCCCGT GATAGATTAA GGAAGACGCC 60
C   ATG TCG CAC GGT GCA AGC AGC CGG CCC GCA ACC GCC CGC AAA TCC 106
    Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser 15
      1      5      10
TCT GGC CTT TCC GGA ACC GTC CGC ATT CCC GGC GAC AAG TCG ATC TCC 154
Ser Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser 30
      20      25
CAC CGG TCC TTC ATG TTC GGC GGT CTC GCG AGC GGT GAA ACG CGC ATC 202
His Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile 45
      35      40
ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC AAT ACG GGC AAG GCC ATG 250
Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met 60
      50      55
CAG GCC ATG GGC GCC AGG ATC CGT AAG GAA GGC GAC ACC TGG ATC ATC 298
Gln Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile 75
      65      70
GAT GGC GTC GGC AAT GGC GGC CTC CTG GCG CCT GAG GCG CCG CTC GAT 346
Asp Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp 95
      80      85

```

Figure 3A

```

394      TTC GGC AAT GCC GCC ACG GGC TGC CGC CTG ACC ATG GGC CTC GTC GGC
      Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly
      100
      110
      115
442      GTC TAC GAT TTC GAC AGC ACC TTC ATC GGC GAC GCC TCG CTC ACA AAG
      Val Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys
      120
      125
490      CGC CCG ATG GGC CGC GTG TTG AAC CCG CTG CGC GAA ATG GGC GTG CAG
      Arg Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln
      130
      135
      140
538      GTG AAA TCG GAA GAC GGT GAC CGT CTT CCC GTT ACC TTG CGC GGC CCG
      Val Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro
      145
      150
      155
586      AAG ACG CCG ACG CCG ATC ACC TAC CGC GTG CCG ATG GCC TCC GCA CAG
      Lys Thr Pro Thr Pro Ile Thr Thr Tyr Arg Val Pro Met Ala Ser Ala Gln
      160
      165
      170
      175
634      GTG AAG TCC GCC GTG CTG CTC GGC GGC CTC AAC ACG CCC GGC ATC ACG
      Val Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr
      180
      185
      190
682      ACG GTC ATC GAG CCG ATC ATG ACG CGC GAT CAT ACG GAA AAG ATG CTG
      Thr Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu
      195
      200
      205

```

Figure 3B

CAG GGC TTT GGC GGC AAC CTT ACC GTC GAG ACG GAT GCG GAC GGC GTG	730
Gln Gly Phe Gly Ala Asn Leu Thr Val Gln Thr Asp Ala Asp Gly Val	
210	
CGC ACC ATC CGC CTG GAA GGC CGC GGC AAG CTC ACC GGC CAA GTC ATC	778
Arg Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile	
225	
230	
235	
GAC GTG CCG GGC GAC CCG TCC TCG ACG GCC TTC CCG CTG GTT GCG GCC	826
Asp Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala	
240	
245	
250	
255	
CTG CTT GTT CCG GGC TCC GAC GTC ACC ATC CTC AAC GTG CTG ATG AAC	874
Leu Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn	
260	
265	
270	
CCC ACC CGC ACC GGC CTC ATC CTG ACG CTG CAG GAA ATG GGC GCC GAC	922
Pro Thr Arg Thr Gly Leu Ile Leu Thr Thr Leu Gln Glu Met Gly Ala Asp	
275	
280	
285	
ATC GAA GTC ATC AAC CCG CGC CTT GCC GGC GGC GAA GAC GTG GCG GAC	970
Ile Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp	
290	
295	
300	
CTG CGC GTT CGC TCC ACC CTG AAG GGC GTC ACG GTG CCG GAA GAC	1018
Leu Arg Val Arg Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp	
305	
310	
315	

Figure 3C

CGC GCG CCT TCG ATG ATC GAC GAA TAT CCG ATT CTC GCT GTC GCC GCC	1066
Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala	335
320	
GCC TTC GCG GAA GGG GCG ACC GTG ATG AAC GGT CTG GAA GAA CTC CGC	1114
Ala Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg	350
340	
GTC AAG GAA AGC GAC CGC CTC TCG GCC GTC GCC AAT GGC CTC AAG CTC	1162
Val Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu	365
355	
AAT GGC GTG GAT TGC GAT GAG GGC GAG AC G TCG CTC GTC GTG CGC GGC	1210
Asn Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly	380
370	
CGC CCT GAC GGC AAG GGG CTC GGC AAC GCC TCG GGC GCC GTC GCC	1258
Arg Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala	395
385	
ACC CAT CTC GAT CAC CGC ATC GCC ATG AGC TTC CTC GTC ATG GGC CTC	1306
Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu	415
400	
GTG TCG GAA AAC CCT GTC ACG GTG GAC GAT GCC ACG ATG ATC GCC ACG	1354
Val Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr	430
420	

Figure 3D

AGC TTC CCG GAG TTC ATG GAC CTG ATG GCC GGG CTG GGC GCG AAG ATC 1402
Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile 445
435 440
GAA CTC TCC GAT ACG AAG GCT GCC TGATGACCTT CACAATCGCC ATCGATGGTC 1456
Glu Leu Ser Asp Thr Lys Ala Ala 455
450
CCGCTGCGGC CGGCAAGGGG ACGCTCTCGC GCCGTATCGC GGAGGTCTAT GGCTTTCATC 1516
ATCTCGATAC GGGCCTGACC TATCGCGCCA CGGCCAAAGC GCTGCTCGAT CGCGGCCTGT 1576
CGCTTGATGA CGAGGCGGTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGGCTCG 1636
ACCGGTCGGT GCTGTGCGGC CATGCCATCG GCGAGGCGGC TTCGAAGATC GCGGTCATGC 1696
CCTCGGTGCG GCGGGCGCTG GTCGAGGCGC AGCGCAGCTT TCGGGCGCGT GAGCCGGGCA 1756
CGGTGCTGGA TGGACGCGAT ATCGGCACGG TGGTCTGCCC GGATGCGCCG GTGAAAGCTCT 1816
ATGTCACCGC GTCACCGGAA GTGCGCGCGA AACGCCGCTA TGACGAAATC CTCGGCAAATG 1876
GCGGGTTGGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGGACA 1936
TGGGTGCGGC GGACAGTCCT TTGAAGCCCCG CCGACGATGC GCACCTT 1982

Figure 3E

GTAGCCACAC ATAATTACTA TAGCTAGGAA GCCCGCTATC TCCTCAATCCC GCGTGATCGC	60
GCCAAAATGT GACTGTGAAA AATCC ATG TCC CAT TCT GCA TCC CCG AAA CCA	112
Met Ser His Ser Ala Ser Pro Lys Pro	
1 5	
GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC ATT CCG	160
Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro	
10 15 20 25	
GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT CTC GCA	208
Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala	
30 35 40	
TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC GTC ATC	256
Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile	
45 50 55	
AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT AAA GAG	304
Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu	
60 65 70	
GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG TTG CAG	352
Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln	
75 80 85	

Figure 4A

400	CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG CGC CTC
	Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu
	90 95 100 105
448	ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT ATC GGC
	Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly
	110 115 120
496	GAC GCC TCG CTG TCG AAG CGC CCG ATG GGC CGC GTG CTG AAC CCG TTG
	Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu
	125 130 135
544	CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC ATG CCG
	Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro
	140 145 150
592	CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT CGC GTG
	Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr Arg Val
	155 160 165
640	CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC GGT CTC
	Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Ala Gly Leu
	170 175 180 185
688	AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC CGC GAC
	Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr Arg Asp
	190 195 200

Figure 4B

CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG GTC GAG 736
His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr Val Glu 215
205 210

ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG GGC AAG 784
Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln Gly Lys 230
220 225

CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG ACC GCC 832
Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser Thr Ala 245
235 240

TTC CCG CTC GTT GCC GCC CTT CTG GTG GAA GGT TCC GAC GTC ACC ATC 880
Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val Thr Ile 260
250 255

CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC ACC TTG 928
Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu 275
270

CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT GCA GGC 976
Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu Ala Gly 290
285

GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC AAG GGC 1024
Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu Lys Gly 300
305 310

Figure 4C

GTC GTC GTT CCG CCG CCG GAA CGT GCG CCG TCG ATG ATC GAC GAA TAT CCG Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro 315 320	1072
GTC CTG GCG ATT GCC GCC TCC TTC GCG GAA ACC GTG ATG GAC Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val Met Asp 330 335 340 345	1120
GGG CTC GAC GAA CTG CCG GTC AAG GAA TCG GAT CGT CTG GCA GCG GTC Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Val 350 355 360	1168
GCA CGC GGC CTT GAA GCC AAC GGC GTC GAT TGC ACC GAA GGC GAG ATG Ala Arg Gly Leu Glu Ala Ala Asn Gly Val Asp Cys Thr Glu Gly Glu Met 365 370 375	1216
TCG CTG ACG GTT CGC GCG CGC CCC GAC GGC AAG GGA CTG GCG GGC GGC Ser Leu Thr Val Arg Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly Gly Gly 380 385 390	1264
ACG GTT GCA ACC CAT CTC GAT CAT CGT ATC GCG ATG AGC TTC CTC GTG Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val 395 400 405	1312
ATG GGC CTT GCG GCG GAA AAG CCG GTG ACG GTT GAC GAC AGT AAC ATG Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser Asn Met 410 415 420 425	1360

Figure 4D

ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA TTG GGC	1408
Ile Ala Thr Ser Phe Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly	
430 435	
GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAA TATTATTTC	1462
Ala Lys Ile Glu Leu Ser Ile Leu	
445	
GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT CTTCCATACG	1522
TAACAGCATC AGGAAATATC AAAAAAGCTT TAGAAGGAAT TGCTAGAGCA GCGACGCCGC	1582
CTAAGCTTTC TCAAGACTTC GTTAAAACTG TACTGAAATC CCGGGGGGTC CGGGGATCAA	1642
ATGACTTCAT TTCTGAGAAA TTGGCCTCGC A	1673

Figure 4E

```

54      GTGATCGCGC CAAAATGTGA CTGTGAAAAA TCC ATG TCC CAT TCT GCA TCC CCG
          Met Ser His Ser Ala Ser Pro
          1           5

102     AAA CCA GCA ACC GCC CGC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC
          Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg
          10      15      20

150     ATT CCG GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT
          Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly
          25      30      35

198     CTC GCA TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC
          Leu Ala Ser Gly Glu Thr Arg Thr Thr Gly Leu Glu Gly Glu Asp
          40      45      50      55

246     GTC ATC AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT
          Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg
          60      65      70

294     AAA GAG GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG
          Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu
          75      80      85

342     TTG CAG CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG
          Leu Gln Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala
          90      95      100

```

Figure 5A

CGC CTC ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT	390
Arg Leu Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe	
105 110 115	
ATC GGC GAC GCC TCG CTG TCG AAG CGC CGC ATG GGC GTG CTG AAC	438
Ile Gly Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn	
120 125 130 135	
CCG TTG CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC	486
Pro Leu Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg	
140 145 150	
ATG CCG CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT	534
Met Pro Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr	
155 160 165	
CGC GTG CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC	582
Arg Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Ala	
170 175 180	
GGT CTC AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC	630
Gly Leu Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr	
185 190 195	
CGC GAC CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG	678
Arg Asp His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr	
200 205 210 215	

Figure 5B

726
GTC GAG ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG
Val Glu Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln
220 225 230

774
GGC AAG CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG
Gly Lys Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser
235 240 245

822
ACC GCC TTC CCG CTC GTT GCC GGC CTT CTG GTG GAA GGT TCC GAC GTC
Thr Ala Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val
250 255 260

870
ACC ATC CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC
Thr Ile Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu
265 270 275

918
ACC TTG CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC CGT CTT
Thr Leu Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu
280 285 290 295

966
GCA GGC GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC
Ala Gly Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu
300 305 310

1014
AAG GGC GTC GTC GTT CCG CCG GAA CGT GCG CCG TCG ATG ATC GAC GAA
Lys Gly Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu
315 320 325

Figure 5C

1062	TAT CCG GTC CTG GCG ATT GCC GCC TTC GCG GAA GGC GAA ACC GTG
	Tyr Pro Val 330 Ala Ile Ala 335 Phe Ala Glu 340 Thr Val
1110	ATG GAC GGG CTC GAC GAA CTG CGC GTC AAG GAA TCG GAT CGT CTG GCA
	Met Asp Gly 345 Leu Asp Glu 350 Arg Val Lys Glu 355 Ser Asp Arg Leu Ala
1158	GGC GTC GCA CGC GGC CTT GAA GCC AAC GGC GTC GAT TGC ACC GAA GGC
	Ala Val Ala Arg Gly 360 Leu Gly 365 Ala Asn Gly 370 Val Asp Cys Thr Glu Gly 375
1206	GAG ATG TCG CTG ACG GTT CGC GGC CGC CCC GAC GGC AAG GGA CTG GGC
	Glu Met Ser Leu 380 Thr Val Arg Gly 385 Arg Pro Asp Gly 390 Lys Gly Leu Gly
1254	GGC GGC ACG GTT GCA ACC CAT CTC GAT CAT CGT ATC GCG ATG AGC TTC
	Gly Gly Thr Val 395 Ala Thr His Leu 400 Asp His Arg Ile Ala Met 405 Ser Phe
1302	CTC GTG ATG GGC CTT GCG GCG GAA AAG CCG GTG ACG GTT GAC GAC AGT
	Leu Val Met Gly 410 Leu Ala Ala Glu 415 Lys Pro Val Thr Val Asp Ser 420
1350	AAC ATG ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA
	Asn Met Ile Ala Thr Ser 425 Phe Pro Glu Phe Met Met Met Pro Gly 430 435

Figure 5D

TTG GGC GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAA	1400
Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu	
440	
445	
TATTATTGCG GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT	1460
CTTCCATACG TAACAGCATC AGGAAATATC AAAAAAGCTT	1500

Figure 5E

[illegible]

Figure 6B

[illegible]

Figure 7B

60 CCATGGCTCA CCGTGCAAGC AGCCGTCCAG CAACTGCTCG TAAGTCCTCT GGTCTTTCTG
120 GAACCGTCCG TATTCCAGGT GACAAGTCTA TCTCCACACAG GTCCTTCATG TTTGGAGGTC
180 TCGCTAGCGG TGAAACTCGT ATCACCGGTC TTTTGGGAAGG TGAAGATGTT ATCAACACTG
240 GTAAGGCTAT GCAAGCTATG GGTGCCAGAA TCCGTAAGGA AGGTGATACT TGGATCATTG
300 ATGGTGTGG TAACGGTGA CTCCTTGCTC CTGAGGCTCC TCTCGATTTC GGTAACGCTG
360 CAACTGGTTG CCGTTTGACT ATGGGTCTTG TTGGTGTTTA CGATTTCGAT AGCACTTTCA
420 TTGGTGACGC TTCTCTCACT AAGCGTCCAA TGGGTCGTGT GTTGAAACCCA CTTCGCGAAA
480 TGGGTGTGCA GGTGAAGTCT GAAGACGGTG ATCGTCTTCC AGTTACCTTG CGTGGACCAA
540 AGACTCCAAAC GCCAATCACC TACAGGGTAC CTATGGCTTC CGCTCAAGTG AAGTCCGCTG
600 TTCTGCTTGC TGGTCTCAAC ACCCCAGGTA TCACCACTGT TATCGAGCCA ATCATGACTC
660 GTGACCACAC TGAAAAGATG CTTCAAGGTT TTGGTGCTAA CCTTACCGTT GAGACTGATG
720 CTGACGGTGT GCGTACCATC CGTCTTGAAG GTCGTGGTAA GCTCACCGGT CAAGTGATTG
780 ATGTTCCAGG TGATCCATCC TCTACTGCTT TCCCATTGGT TGCTGCCCTG CTTGTTCCAG
840 GTTCCGACGT CACCATCCTT AACGTTTGA TGAACCCAAC CCGTACTGGT CTCATCTTGA

Figure 8A

CTCTGCAGGA AATGGGTGCC GACATCGAAG TGATCAACCC ACGTCTTGCT GGTGAGAAG	900
ACGTGGCTGA CTTCGGTGTT CGTCTTCTA CTTTGAAGGG TGTACTGTT CCAGAAAGACC	960
GTGCTCCTTC TATGATCGAC GAGTATCCAA TTCTCGCTGT TGCAGCTGCA TTCGCTGAAG	1020
GTGCTACCGT TATGAACGGT TTGGAAGAAC TCCGTGTAA GGAAAGCGAC CGTCTTCTG	1080
CTGTCGCAA CCGTCTCAAG CTCAACGGTG TTGATTGCGA TGAAGGTGAG ACTTCTCTCG	1140
TCGTGCGTGG TCGTCCTGAC GGTAAGGGTC TCGGTAAAGC TTCTGGAGCA GCTGTCGCTA	1200
CCCACCTCGA TCACCGTATC GCTATGAGCT TCCTCGTTAT GGGTCTCGTT TCTGAAAACC	1260
CTGTTACTGT TGATGATGCT ACTATGATCG CTACTAGCTT CCCAGAGTTC ATGGATTGA	1320
TGGCTGGTCT TGGAGCTAAG ATCGAACTCT CCGACACTAA GGCTGCTTGA TGAGCTC	1377

Figure 8B

AGATCTATCG	ATAAGCTTGA	TGTAATTGGA	GGAAGATCAA	AATTTTCAAT	CCCCATTCCTT	60
CGATTGCTTC	AATTGAAGTT	TCTCCG	ATG GCG CAA	GTT AGC AGA	ATC TGC AAT	113
	Met	Ala	Gln	Val	Ser Arg Ile	Cys Asn
	1			5		
GGT GTG	CAG AAC	CCA TCT	CTT ATC	TCC AAT	CTC TCG AAA	TCC AGT CAA
Gly Val	Gln Asn	Pro Ser	Leu Ile	Ser Asn	Leu Ser	Lys Ser Gln
10	15	20	25			
CGC AAA	TCT CCC	TTA TCG	GTT TCT	CTG AAG	ACG CAG CAG	CAT CCA CGA
Arg Lys	Ser Pro	Leu Pro	Ser Leu	Ser Lys	Thr Gln	His Pro Arg
	30	35	40			
GCT TAT	CCG ATT	TCG TCG	TGG GGA	TTG AAG	AAG AGT	GGG ATG ACG
Ala Tyr	Pro Ile	Ser Ser	Trp Gly	Leu Lys	Ser Gly	Met Thr
	45	50	55			
TTA ATT	GGC TCT	GAG CTT	CGT CCT	CTT AAG	GTC ATG	TCT TCT GTT TCC
Leu Ile	Gly Ser	Glu Leu	Arg Pro	Leu Lys	Val Met	Ser Ser Val Ser
	60	65	70			
ACG GCG	TGC ATG	C				
Thr Ala	Cys Met					
	75					

Figure 9

AGATCTATCG	ATAAGCTTGA	TGTAATTGGA	GGAAGATCAA	AATTTTCAAT	CCCCATTC	TT	60
CGATTGCTTC	AATTGAAGTT	TCTCCG	ATG GCG CAA	GTT AGC AGA	ATC TGC AAT		113
	Met Ala Gln	Val Ser Arg	Ile Cys Asn				
	1		5				
GGT GTG CAG AAC CCA	TCT CTT ATC	TCC AAT CTC	TCG AAA TCC	AGT CAA			161
Gly Val Gln Asn Pro	Ser Leu Ile Ser	Asn Leu Ser	Lys Ser Ser	Gln	25		
	10	15	20				
CGC AAA TCT CCC TTA	TCG GTT TCT	CTG AAG ACG	CAG CAG CAT	CCA CGA			209
Arg Lys Ser Pro Leu	Ser Val Ser Leu	Lys Thr Gln	Gln His Pro	Arg	40		
	30	35					
GCT TAT CCG ATT TCG	TCG TCG TCG	TGG GGA TTG	AAG AAG AGT	GGG ATG	ACG		257
Ala Tyr Pro Ile Ser	Ser Ser Trp Gly	Leu Lys Ser	Gly Met Thr				
	45	50	55				

Figure 10A

TTA	ATT	GGC	TCT	GAG	CTT	CGT	CCT	CTT	AAG	GTC	ATG	TCT	TCT	GTT	TCC	305
Leu	Ile	Gly	Ser	Glu	Leu	Arg	Pro	Leu	Lys	Val	Met	Ser	Ser	Val	Ser	
		60					65					70				
ACG	GCG	GAG	AAA	GCG	TCG	GAG	ATT	GTA	CTT	CAA	CCC	ATT	AGA	GAA	ATC	353
Thr	Ala	Glu	Lys	Ala	Ser	Glu	Ile	Val	Leu	Gln	Pro	Ile	Arg	Glu	Ile	
		75				80					85					
TCC	GGT	CTT	ATT	AAG	TTG	CCT	GGC	TCC	AAG	TCT	CTA	TCA	AAT	AGA	ATT	401
Ser	Gly	Leu	Ile	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	Arg	Ile	
90					95					100					105	
C																402

Figure 10B

AGATCTTCA AGA ATG GCA CAA ATT AAC AAC ATG GCT CAA GGG ATA CAA	49
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln	
1 5 10	
ACC CTT AAT CCC AAT TCC AAT TTC CAT AAA CCC CAA GTT CCT AAA TCT	97
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser	
15 20 25	
TCA AGT TTT CTT GTT TTT GGA TCT AAA AAA CTG AAA AAT TCA GCA AAT	145
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn	
30 35 40	
TCT ATG TTG GTT TTG AAA AAA GAT TCA ATT TTT ATG CAA AAG TTT TGT	193
Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys	
45 50 55 60	
TCC TTT AGG ATT TCA GCA TCA GTG GCT ACA GCC TGC ATG C	233
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met	
65 70	

Figure 11

AGATCTGCTA GAAATAATTT TGTTTAACTT TAAGAAGGAG ATATATCC ATG GCA CAA	57
Met Ala Gln	
1	
ATT AAC AAC ATG GCT CAA GGG ATA CAA ACC CTT AAT CCC AAT TCC AAT	105
Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro Asn Ser Asn	
5 10 15	
TTC CAT AAA CCC CAA GTT CCT AAA TCT TCA AGT TTT CTT GTT TTT GGA	153
Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu Val Phe Gly	
20 25 30 35	
TCT AAA AAA CTG AAA AAT TCA GCA AAT TCT ATG TTG GTT TTG AAA AAA	201
Ser Lys Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val Leu Lys Lys	
40 45 50	

Figure 12A

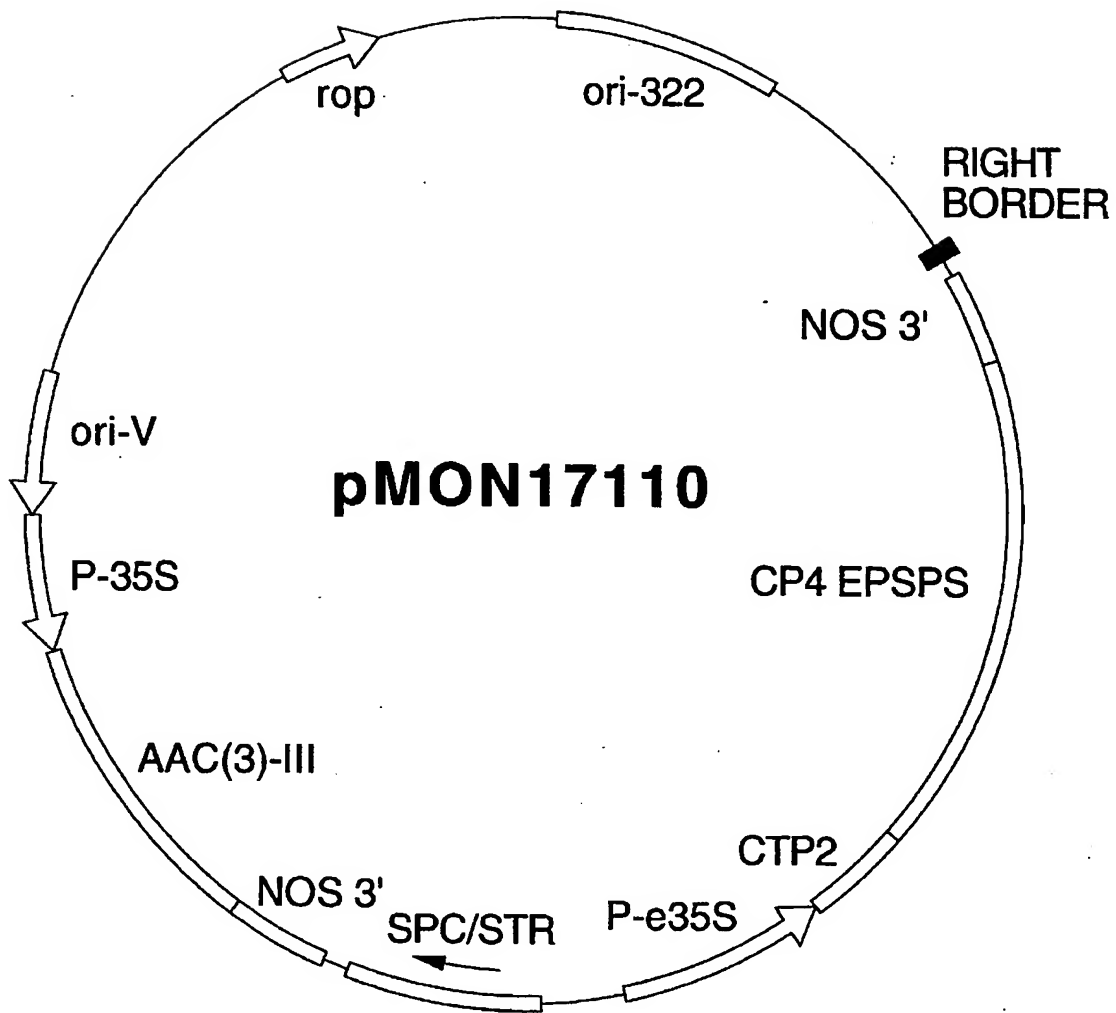


Figure 13

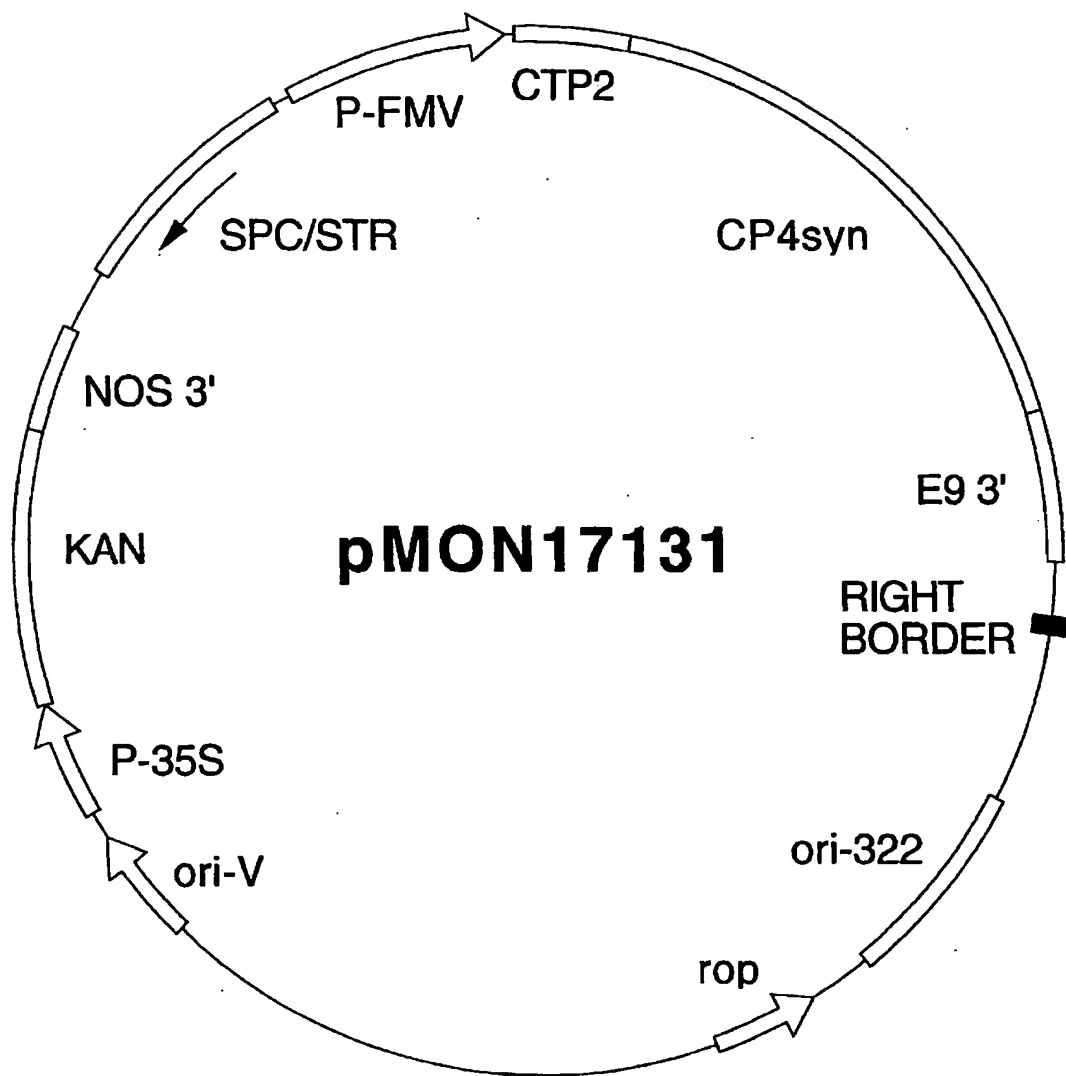
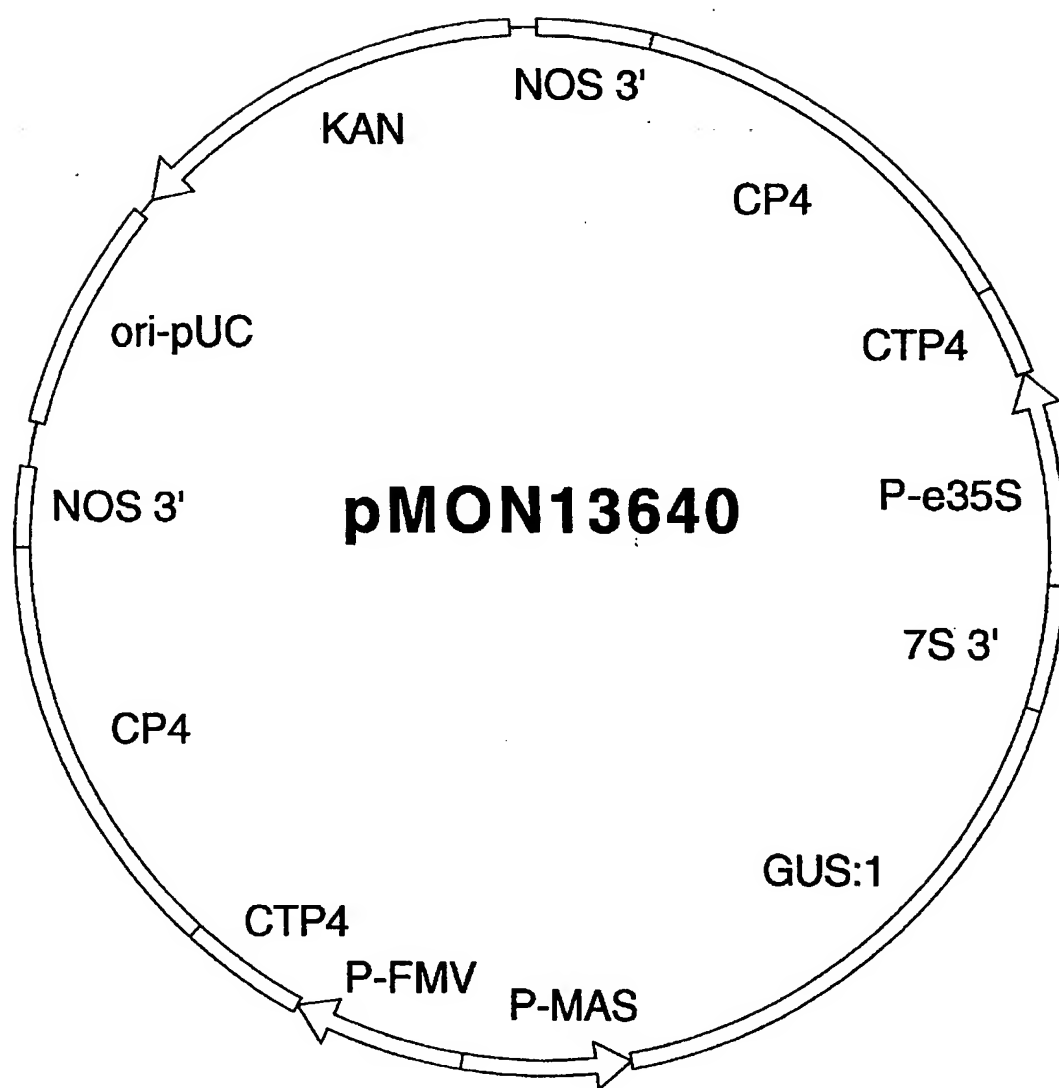
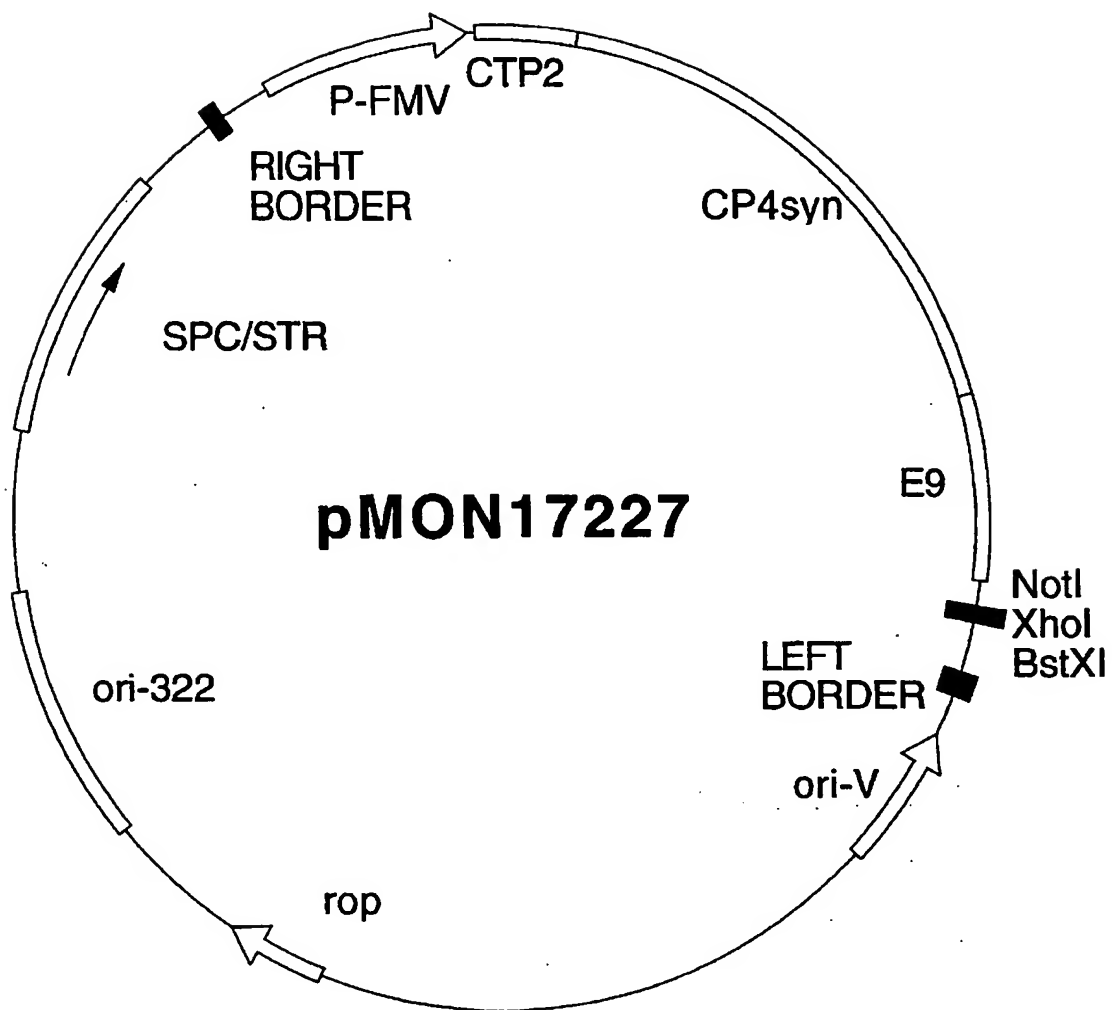


Figure 14

**Figure 15**

**Figure 16**

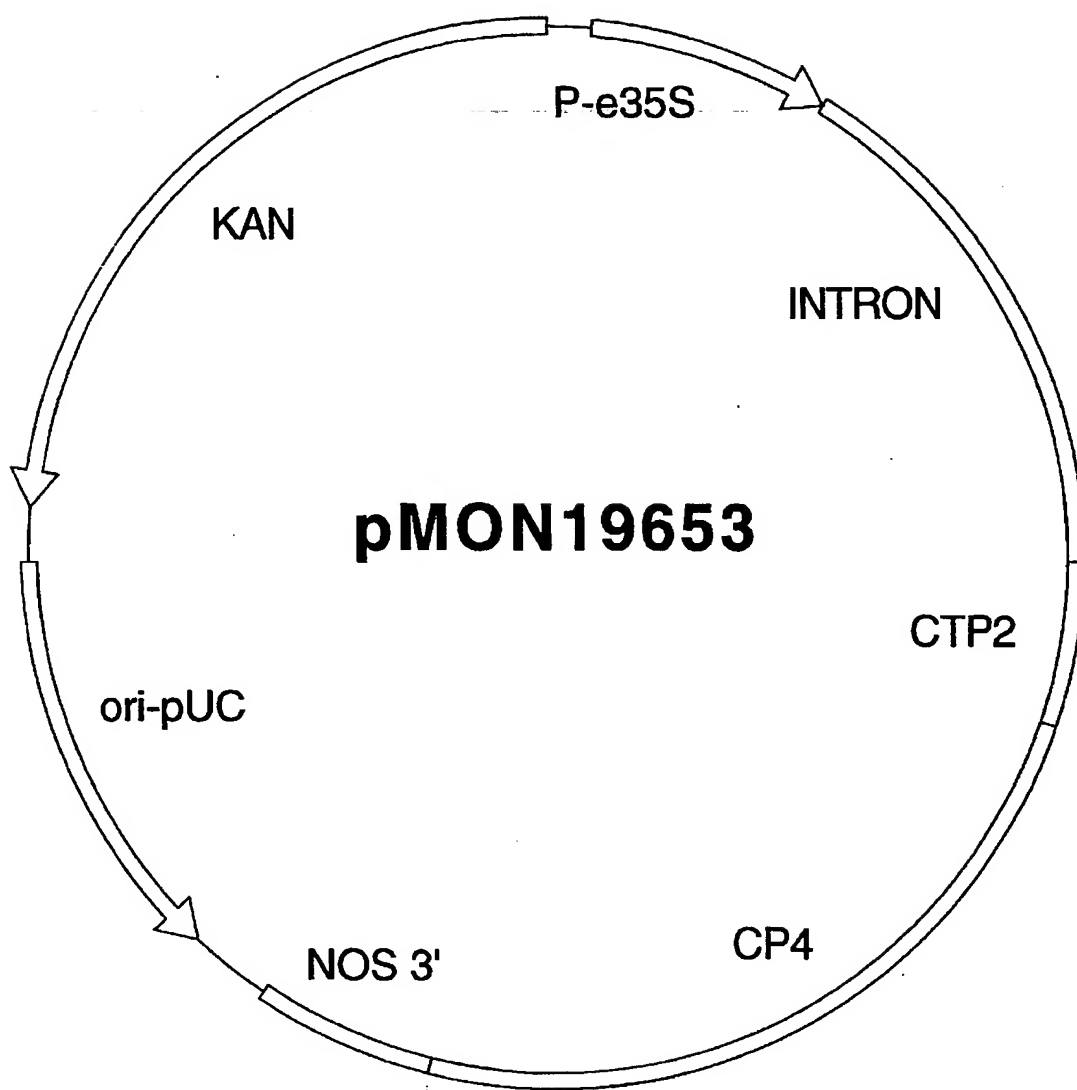


Figure 17

```

48      ATG AAA CGA GAT AAG GTG CAG ACC TTA CAT GGA GAA ATA CAT ATT CCC
      Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro
      1      5      10      15

96      GGT GAT AAA TCC ATT TCT CAC CGC TCT GTT ATG TTT GGC GCG CTA GCG
      Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala
      20      25      30

144     GCA GGC ACA ACA ACA GTT AAA AAC TTT CTG CCG GGA GCA GAT TGT CTG
      Ala Gly Thr Thr Thr Val Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu
      35      40      45

192     AGC ACG ATC GAT TGC TTT AGA AAA ATG GGT GTT CAC ATT GAG CAA AGC
      Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser
      50      55      60

240     AGC AGC GAT GTC GTG ATT CAC GGA AAA GGA ATC GAT GCC CTG AAA GAG
      Ser Ser Asp Val Val Ile Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu
      65      70      75      80

288     CCA GAA AGC CTT TTA GAT GTC GGA AAT TCA GGT ACA ACG ATT CGC CTG
      Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu
      85      90      95

336     ATG CTC GGA ATA TTG GCG GGC CGT CCT TTT TAC AGC GCG GTA GCC GGA
      Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly
      100      105      110

```

Figure 18A

384 GAT GAG AGC ATT GCG AAA CGC CCA ATG AAG CGT GTG ACT GAG CCT TTG
 Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu
 115 120 125
 432 AAA AAA ATG GGG GCT AAA ATC GAC GGC AGA GCC GGA GAG TTT ACA
 Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Glu Phe Thr
 130 135 140
 480 CCG CTG TCA GTG AGC GGC GCT TCA TTA AAA GGA ATT GAT TAT GTA TCA
 Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser
 145 150 155 160
 528 CCT GTT GCA AGC GCG CAA ATT AAA TCT GCT GTT TTG CTG GCC GGA TTA
 Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Ala Gly Leu
 165 170 175
 576 CAG GCT GAG GGC ACA ACT GTA ACA GAG CCC CAT AAA TCT CGG GAC
 Gln Ala Glu Gly Thr Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp
 180 185 190
 624 CAC ACT GAG CGG ATG CTT TCT GCT TTT GGC GTT AAG CTT TCT GAA GAT
 His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp
 195 200 205
 672 CAA ACG AGT GTT TCC ATT GCT GGT GGC CAG AAA CTG ACA GCT GCT GAT
 Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp
 210 215 220

Figure 18B

ATT TTT GTT CCT GGA GAC ATT TCT TCA GCC GCG TTT TTC CTT GCT GCT	720
Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala	240
225	
GGC GCG ATG GTT CCA AAC AGC AGA ATT GTA TTG AAA AAC GTA GGT TTA	768
Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu	255
245	
AAT CCG ACT CGG ACA GGT ATT ATT GAT GTC CTT CAA AAC ATG GGG GCA	816
Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala	270
265	
AAA CTT GAA ATC AAA CCA TCT GCT GAT AGC GGT GCA GAG CCT TAT GGA	864
Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly	285
275	
GAT TTG ATT ATA GAA ACG TCA TCT CTA AAG GCA GTT GAA ATC GGA GGA	912
Asp Leu Ile Ile Glu Thr Ser Ser Ser Leu Lys Ala Val Glu Ile Gly Gly	300
290	
GAT ATC ATT CCG CGT TTA ATT GAT GAG ATC CCT ATC ATC GCG CTT CTT	960
Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu	315
305	
GGC ACT CAG GCG GAA GGA ACC ACC GTT ATT AAG GAC GCG GCA GAG CTA	1008
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu	330
325	
335	

Figure 18C

AAA GTG AAA GAA ACA AAC CGT ATT GAT ACT GTT GTT TCT GAG CTT CGC	1056
Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Ser Glu Leu Arg	
340	345
AAG CTG GGT GCT GAA ATT GAA CCG ACA GCA GAT GGA ATG AAG GTT TAT	1104
Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr	
355	360
GGC AAA CAA ACG TTG AAA GGC GGC GCT GCA GTG TCC AGC CAC GGA GAT	1152
Gly Lys Gln Thr Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp	
370	375
CAT CGA ATC GGA ATG ATG ATG CTT GGT ATT GCT TCC TGT ATA ACG GAG GAG	1200
His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu	
385	390
CCG ATT GAA ATC GAG CAC CAC GAT GCC ATT CAC GAT GTT TCT TAT CCA ACC	1248
Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr	
405	410
TTC TTC GAG CAT TTA AAT AAG CTT TCG AAA AAA TCC TGA	1287
Phe Phe Glu His Leu Asn Lys Lys Ser Lys Lys Ser	
420	425

Figure 18D

ATG GTA AAT GAA CAA ATC ATT GAT ATT TCA GGT CCG TTA AAG GGC GAA	48
Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu	15
1	
5	
10	
ATA GAA GTG CCG GGC GAT AAG TCA ATG ACA CAC CGT GCA ATC ATG TTG	96
Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu	30
20	
25	
35	
40	
45	
50	
55	
60	
65	
70	
75	
80	
85	
90	
95	
100	
105	
110	
115	
120	
125	
130	
135	
140	
145	
150	
155	
160	
165	
170	
175	
180	
185	
190	
195	
200	
205	
210	
215	
220	
225	
230	
235	
240	
245	
250	
255	
260	
265	
270	
275	
280	
285	
290	
295	
300	
305	
310	
315	
320	
325	
330	
335	
340	
345	
350	
355	
360	
365	
370	
375	
380	
385	
390	
395	
400	
405	
410	
415	
420	
425	
430	
435	
440	
445	
450	
455	
460	
465	
470	
475	
480	
485	
490	
495	
500	
505	
510	
515	
520	
525	
530	
535	
540	
545	
550	
555	
560	
565	
570	
575	
580	
585	
590	
595	
600	
605	
610	
615	
620	
625	
630	
635	
640	
645	
650	
655	
660	
665	
670	
675	
680	
685	
690	
695	
700	
705	
710	
715	
720	
725	
730	
735	
740	
745	
750	
755	
760	
765	
770	
775	
780	
785	
790	
795	
800	
805	
810	
815	
820	
825	
830	
835	
840	
845	
850	
855	
860	
865	
870	
875	
880	
885	
890	
895	
900	
905	
910	
915	
920	
925	
930	
935	
940	
945	
950	
955	
960	
965	
970	
975	
980	
985	
990	
995	
1000	

Figure 19A

TTG TCT GGC GAT GTT TCA ATT GGT AAA AGG CCA ATG GAT CGT GTC TTG	384
Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu	
	115
	120
	125
AGA CCA TTG AAA CTT ATG GAT GCG AAT ATT GAA GGT ATT GAA GAT AAT	432
Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn	
	130
	135
	140
TAT ACA CCA TTA ATT ATT AAG CCA TCT GTC ATA AAA GGT ATA AAT TAT	480
Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr	
	145
	150
	155
CAA ATG GAA GTT GCA AGT GCA CAA GTA AAA AGT GCC ATT TTA TTT GCA	528
Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala	
	165
	170
	175
AGT TTG TTT TCT AAG GAA CCG ACC ATC ATT AAA GAA TTA GAT GTA AGT	576
Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser	
	180
	185
	190
CGA AAT CAT ACT GAG ACG ATG TTC AAA CAT TTT AAT ATT CCA ATT GAA	624
Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu	
	195
	200
	205
GCA GAA GGG TTA TCA ATT AAT ACA ACC CCT GAA GCA ATT CGA TAC ATT	672
Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile	
	210
	215
	220

Figure 19B

AAA CCT GCA GAT TTT CAT GTT CCT GGC GAT ATT TCA TCT GCA GCG TTC	720
Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe	
225 230 235 240	
TTT ATT GTT GCA GCA CTT ATC ACA CCA GGA AGT GAT GTA ACA ATT CAT	768
phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His	
245 250 255	
AAT GTT GGA ATC AAT CAA ACA CGT TCA GGT ATT ATT GAT ATT GTT GAA	816
Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu	
260 265 270	
AAA ATG GGC GGT AAT ATC CAA CTT TTC AAT CAA ACA ACT GGT GCT GAA	864
Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu	
275 280 285	
CCT ACT GCT TCT ATT CGT ATT CAA TAC ACA CCA ATG CTT CAA CCA ATA	912
Pro Thr Ala Ser Ile Arg Ile Gln Thr Tyr Thr Pro Met Leu Gln Pro Ile	
290 295 300	
ACA ATC GAA GGA GAA TTA GTT CCA AAA GCA ATT GAT GAA CTG CCT GTA	960
Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val	
305 310 315 320	
ATA GCA TTA CTT TGT ACA CAA GCA GTT GGC ACG AGT ACA ATT AAA GAT	1008
Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp	
325 330 335	

Figure 19C

GCC GAG GAA TTA AAA GTA AAA GAA ACA AAT AGA ATT GAT ACA ACG GCT Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala 340 345 350	1056
GAT ATG TTA AAC TTG TTA TTA GGG TTT GAA TTA CAA CCA ACT AAT GAT GGA Asp Met Leu Asn Leu Leu Leu Phe Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly 355 360 365	1104
TTG ATT ATT CAT CCG TCA GAA TTT AAA ACA AAT GCA ACA GAT ATT TTA Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu 370 375 380	1152
ACT GAT CAT CGA ATA GGA ATG ATG CTT GCA GTT GCT TGT GTA CTT TCA Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser 385 390 395	1200
AGC GAG CCT GTC AAA ATC AAA CAA TTT GAT GCT GTA AAT GTA TCA TTT Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe 400 405 410 415	1248
CCA GGA TTT TTA CCA AAA CTA AAG CTT TTA CAA AAT GAG GGA TAA Pro Gly Phe Leu Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly 420 425 430	1293

Figure 19D

PG2982	51	100
LBAA	EIRIPGDKSI	SHRSFMFGGL ASGETRITGL LEGEDVINTG RAMQAM.GAK
Agrobacterium CP4	EIRIPGDKSI	SHRSFMFGGL ASGETRITGL LEGEDVINTG RAMQAM.GAK
B. subtilis	TVRIPGDKSI	SHRSFMFGGL ASGETRITGL LEGEDVINTG KAMQAM.GAR
S. aureus	EIHIPGDKSI	SHRSVMFGAL AAGTTVKNF LPGADECLSTI DCFRKM.GVH
S. cerevisiae	EIEVPGDKSM	THRAIMLASL AEGVSTIYKP LLGEDCRRTM DIFRHL.GVE
A. nidulans	VVIPGSKSI	SNRALILAAAL GEGQCKIKNL LHSDDTKHML TAVHELKGAT
B. napus	ICAPPGSKSI	SNRALVLAAL GSGTCRIKNL LHSDDTVVML NALERLGAAT
A. thaliana	LIKLPGSKSL	SNRIILLLAAL SEGTTVVDNL LNSDDINYML DALKKL.GLN
N. tabacum	LIKLPGSKSL	SNRIILLLAAL SEGTTVVDNL LNSDDINYML DALKRL.GLN
L. esculentum	TVKLPGSKSL	SNRIILLLAAL SKGRTVVDNL LSSDDIHYML GALKTL.GLH
P. hybrida	TVKLPGSKSL	SNRIILLLAAL SEGTTVVDNL LSSDDIHYML GALKTL.GLH
Z. mays	TVKLPGSKSL	SNRIILLLAAL SEGTTVVDNL LSSDDIHYML GALKTL.GLH
S. gallinarum	AINLPGSKSV	SNRALLLAAL ACCKTVLTNL LDSDDVRHML NALSAL.GIN
S. typhimurium	AINLPGSKSV	SNRALLLAAL PCGKTALTNL LDSDDVRHML NALSAL.GIN
S. typhi	AINLPGSKSV	SNRALLLAAL ACCKTVLTNL LDSDDVRHML NALSAL.GIN
E. coli	TINLPGSKTV	SNRALLLAAL AHGKTVLTNL LDSDDVRHML NALTAL.GVS
K. pneumoniae	TVNLPGSKSV	SNRALLLAAL ARGTTVLTNL LDSDDVRHML NALSAL.GVH
Y. enterocolitica	TVNLPGSKSV	SNRALLLAAL AEGTTQLNNL LDSDDIRHML NALQAL.GVK
H. influenzae	TINLPGSKSL	SNRALLLAAL AKGTTKVTNL LDSDDIRHML NALKAL.GVR
P. multocida	EVRLPGSKSL	SNRALLLSAL AKGTTTLTNL LDSDDVRHML NALKEL.GVT
A. salmonicida	EVNLPGSKSV	SNRALLLAAL ARGTTTLTNL LDSDDIRHML AALTQL.GVK
B. pertussis	EVALPGSKSI	SNRVLLLAAL AEGSTEITGL LDSDDTRVML AALRQL.GVS
Consensus	----PG-K--	--R-----L --G-----L-----D-----

Figure 20B

PG2982	101	IRKEGDVWII	NGVNGCCLLQ	P.....EAA	LDFGNAGTGA	RLTMGLVGTY	150
LBAA		IRKEGDVWII	NGVNGCCLLQ	P.....EAA	LDFGNAGTGA	RLTMGLVGTY	
Agrobacterium CP4		IRKEGDTWII	DGVNGGGLLA	P.....EAP	LDFGNAATGC	RLTMGLVGVY	
B. subtilis		IEQSSSDVVI	HGKGIDALKE	P.....ESL	LDVNSGTTI	RLMLGILAGR	
S. aureus		IKEDDEKLIV	TSPGYQ.VNT	P.....HQV	LYTNSGTTT	RLLAGLLSGL	
S. cerevisiae		ISWEDNGETV	VVEGHGG...	.STLSACADP	LYLGNAGTAS	RFLTSLAALV	
A. nidulans		FSWEEEGEVL	VVNGKGG...	..NLQASSP	LYLGNAGTAS	RFLTTVATLA	
B. napus		VERDSVNNRA	VVEGCGGIFP	ASLDSKSDIE	LYLGNAGTAM	RPLTAAAVTAA	
A. thaliana		VETDSENNRA	VVEGCGGIFP	ASIDSKSDIE	LYLGNAGTAM	RPLTAAAVTAA	
N. tabacum		VEDDNEENQRA	IVEGCGGQFP	VGKKSEEEIQ	LFLGNAGTAM	RPLTAAAVTVA	
L. esculentum		VEDDNEENQRA	IVEGCGGQFP	VGKKSEEEIQ	LFLGNAGTAM	RPLTAAAVTVA	
P. hybrida		VEEDSANQRA	VVEGCGGLFP	VGKESKEEIQ	LFLGNAGTAM	RPLTAAAVTVA	
Z. mays		VEADKAAKRA	VVVGCGGKFP	VE.DAKEEVQ	LFLGNAGTAM	RPLTAAAVTAA	
S. gallinarum		YTLSDRTRC	DITNGGGPLR	AP....GALE	LFLGNAGTAM	RPLAAALCL.	
S. typhimurium		YTLSDRTRC	DITNGGGALR	AP....GALE	LFLGNAGTAM	RPLAAALCL.	
S. typhi		YTLSDRTRC	DITNGGGPLR	AS....GTLE	LFLGNAGTAM	RPLAAALCL.	
E. coli		YTLSDRTRC	EIINGGGPLH	AE....GALE	LFLGNAGTAM	RPLAAALCL.	
K. pneumoniae		YVLSSDRTRC	EVTGTGGPLQ	AG....SALE	LFLGNAGTAM	RPLAAALCL.	
Y. enterocolitica		YRLSADRTRC	EVDGLGKLV	AE....QPLE	LFLGNAGTAM	RPLAAALCL.	
H. influenzae		YQLSDDKTIC	EIEGLGAFN	IQ....DNLS	LFLGNAGTAM	RPLTAAALCLK	
P. multocida		YQLSEDKSVC	EIEGLGRAFE	WQ....SGLA	LFLGNAGTAM	RPLTAAALCLS	
A. salmonicida		YKLSADKTEC	TVHGLGRSFA	VS....APVN	LFLGNAGTAM	RPLCAALCL.	
B. pertussis		VGEVAD..GC	VTIEGVARFP	TE.....QAE	LFLGNAGTAF	RPLTAAALAM	
Consensus		-----	-----	-----	L--GN--T--	R-----	

Figure 20C

151	PG2982	DM.....KT	SFIGDASLSK	RPMGRVLNPL	REMGVQVEAA	DGDRMPLT..	200
	LBAA	DM.....KT	SFIGDASLSK	RPMGRVLNPL	REMGVQVEAA	DGDRMPLT..	
	Agrobacterium CP4	DF.....DS	TFIGDASLTK	RPMGRVLNPL	REMGVQVKSE	DGDRLPVT..	
	B. subtilis	PF.....YS	AVAGDESIK	RPMKRVTEPL	KKMGAKIDGR	AGGEFTPL..	
	S. aureus	GN.....ES	VLSGDSVIGK	RPMDRVLRPL	KLMDANIEG.	IEDNYTPL..	
	S. cerevisiae	NST.SSQYI	VLGTGNARMQ	RPIAPLVDSL	RANGTKIEYL	NNEGSLPIKV	
	A. nidulans	NS...STVDSS	VLGTGNRMKQ	RPIGDLVDAL	TANVLPLNTS	KGRASLPLKI	
	B. napus	G....GNASY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVECT	LGTNCPVVRV	
	A. thaliana	G....GNASY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVECT	LGTNCPVVRV	
	N. tabacum	G....GHSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCF	LGTNCPVRI	
	L. esculentum	G....GHSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCS	LGTNCPVRI	
	P. hybrida	G....GNSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCF	LGTNCPVRI	
	Z. mays	G....GNATY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVDCF	LGTDCPPVRV	
	S. gallinarumGQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPRLRL	
	S. typhimuriumGQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPRLRL	
	S. typhiGQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPRLRL	
	E. coliGSNDI	VLTEPRMKE	RPIGHLVDAL	RLGGAKITYL	EQENYPPRLRL	
	K. pneumoniaeGSNDI	VLTEPRMKE	RPIGHLVDAL	RQGGAQIDYL	EQENYPPRLRL	
	Y. enterocoliticaGKNDI	VLTEPRMKE	RPIGHLVDAL	RQGGAQIDYL	EQENYRR.CI	
	H. influenzae	G.NHEV..EI	ILTGEPRMKE	RPILHLVDAL	RQAGADIRYL	ENEGYPPPLAI	
	P. multocida	TPNREGKNEI	VLTEPRMKE	RPIQHLVDAL	CQAGAEIQYL	EQEGYPPPIAI	
	A. salmonicidaGSGEY	MLGGEPRMEE	RPIGHLVDCL	ALKGAGHIQYL	KKDGYPPPLV	
	B. pertussis	G.....GDY	RLSGVPRMHE	RPIGDLVDAL	RQFGAGIEYL	GQAGYPPPLRI	
	Consensus	-----G-----	RP-----L				

Figure 20D

PG2982	201	LIGPK	TANPITYRVP	MASQVKS	AV	LLAGLN	250	TPGVTT
LBAA		LIGPK	TANPITYRVP	MASQVKS	AV	LLAGLN		TPGVTT
Agrobacterium CP4		LRGPK	TPPITYRVP	MASQVKS	AV	LLAGLN		TPGITT
B. subtilis		SVSGA	SLKGIDYVSP	VASAQIKS	AV	LLAGLQ		AEGTTT
S. aureus		IIKPS	VIKGINYQME	VASQVKS	AI	LFASLF		SKEPTI
S. cerevisiae		YTDSVFKG	..	GRIELAA	TVSSQYVSSI	LMCAPYAE		EPVTLALVG
A. nidulans		AASGGFAG	..	GNINLAA	KVSSQYVSSL	LMCAPYAK		EPVTLRLVG
B. napus		NANGGLPG	..	GKVKLSG	SISSQYLTL	LMAAP.LA		LGDVEIEII
A. thaliana		NANGGLPG	..	GKVKLSG	SISSQYLTL	LMSAP.LA		LGDVEIEIV
N. tabacum		VSKGGLPG	..	GKVKLSG	SISSQYLTL	LMAAP.LA		LGDVEIEII
L. esculentum		VSKGGLPG	..	GKVKLSG	SISSQYLTL	LMAAP.LA		LGDVEIEII
P. hybrida		VSKGGLPG	..	GKVKLSG	SISSQYLTL	LMAAP.LA		LGDVEIEII
Z. mays		NGIGGLPG	..	GKVKLSG	SISSQYLSAL	LMAAP.LP		LGDVEIEII
S. gallinarum		RG..GFIG	..	GDIKVDG	SVSSQFLTL	LMTAP.LA		PKDTIIRVK
S. typhimurium		RG..GFTG	..	GDIKVDG	SVSSQFLTL	LMTAP.LA		PKDTIIRVK
S. typhi		RG..GFIG	..	GDIKVDG	SVSSQFLTL	LMTAP.LA		PEDTIIIRVK
E. coli		QG..GFTG	..	GNVDVDG	SVSSQFLTL	LMTAP.LA		PEDTVIRIK
K. pneumoniae		RG..GFTG	..	GDIKVDG	SVSSQFLTL	LMAAP.LA		PQDTVIAIK
Y. enterocolitica		AG..GFRG	..	GKLTVDG	SVSSQFLTL	LMTAP.LA		EQDTEIQIQ
H. influenzae		RNK.GIKG	..	GKVKIDG	SISSQFLTL	LMSAP.LA		ENDTEIEII
P. multocida		RNT.GLKG	..	GRIQIDG	SVSSQFLTL	LMAAP.MA		EADTEIEII
A. salmonicida		DAK.GLWG	..	GDVHVDG	SVSSQFLTAF	LMAAPAMA		PVIPRIHIK
B. pertussis		GGGSIRVD	..	GPVRVEG	SVSSQFLTL	LMAAPVLARR		SGQDITIEV
Consensus		-----	-----	-----	-----S-Q-----	-----L-----		-----

Figure 20E

PG2982	251	VIEPVMTRDH	TEKMLQGFGA	DLTVETDKDG	VRHIRTGGQ	KLVGQ.TIDV	300
LBAA		VIEPVMTRDH	TEKMLQGFGA	DLTVETDKDG	VRHIRTGGQ	KLVGQ.TIDV	
Agrobacterium CP4		VIEPIMTRDH	TEKMLQGFGA	NLTVETDADG	VRTIRLEGRG	KLTDG.VIDV	
B. subtilis		VTEPHKSRDH	TERMLSAFGV	KLSEDQTS..	..VSIAGGQ	KLTA.DIFV	
S. aureus		IKELDVSRNH	TETMFKHFN	PIEAEGLS..	..INTTPEAI	RYIKPADFHV	
S. cerevisiae		GKPISKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI	
A. nidulans		GKPISQPYID	MTTAMMRSFG	ID..VQSTT	EEHTYHIPQG	RYVNPAEYVI	
B. napus		DKLISVPYVE	MTLKLMEFRG	VS..AEHSDS	WDRFFVKGQ	KYKSPGNAYV	
A. thaliana		DKLISVPYVE	MTLKLMEFRG	VS..VEHSDS	WDRFFVKGQ	KYKSPGNAYV	
N. tabacum		DKLISVPYVE	MTLKLMEFRG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV	
L. esculentum		DKLISVPYVE	MTLKLMEFRG	VF..VEHSSG	WDRFLVKGQ	KYKSPGKAFV	
P. hybrida		DKLISVPYVE	MTLKLMEFRG	IS..VEHSSS	WDRFFVVRGGQ	KYKSPGKAFV	
Z. mays		DKLISIPYVE	MTLRLMEFRG	VK..AEHSDS	WDRFYIKGGQ	KYKSPKNAYV	
S. gallinarum		GELVSKPYID	ITLNLTKTFF	VE..IAN.HH	YQFVVKGGQ	QYHSPGRYLV	
S. typhimurium		GELVSKPYID	ITLNLTKTFF	VE..IAN.HH	YQFVVKGGQ	QYHSPGRYLV	
S. typhi		GELVSKPYID	ITLNLTKTFF	VE..IAN.HH	YQFVVKGGQ	QYHSPGRYLV	
E. coli		GDLVSKPYID	ITLNLTKTFF	VE..IEN.QH	YQFVVKGGQ	SYQSPGTLYV	
K. pneumoniae		GELVSRPYID	ITLHLTKTFF	VE..VEN.QA	YQRFIVRGQ	QYQSPGDYLV	
Y. enterocolitica		GELVSKPYID	ITLHLMKAFG	VD..VVH.EN	YQIFHIKGGQ	TYRSPGIYLV	
H. influenzae		GELVSKPYID	ITLAMMRDFG	VK..VEN.HH	YQKFQVKGQ	SYISPNKYLV	
P. multocida		GELVSKPYID	ITLKMMDTFF	VE..VEN.QA	YQRFVKGHQ	QYQSPHRFLV	
A. salmonicida		GELVSKPYID	ITLHIMNSSG	VV..IEH.DN	YKLFYIKGNQ	SIVSPGDFLV	
B. pertussis		GELISKPYIE	ITLNLMARFG	VS..V.RRDG	WRAFTIARDA	VYRGPGRMAI	
Consensus		-----	-----	-----	-----	-----	

Figure 20F

PG2982	PGDPSSTAFF	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	350
LBAA	PGDPSSTAFF	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	
Agrobacterium CP4	PGDPSSTAFF	LVAALLVPGS	DVTILNVLMN	PTRTGL...	I	LTLQEMGADI	
B. subtilis	PGDISSAAFF	LAAGAMVPNS	RIVLKNVGLN	PTRTGI...	I	DVLQNMGAKL	
S. aureus	PGDISSAAFF	IVAALITPGS	DVTIHNVGIN	QTRSGI...	I	DIVEKMGGNI	
S. cerevisiae	ESDASSATYP	LAFAA.MTGT	TVTVPNIGFE	SLQGDARFAR		DVLKPMGCKI	
A. nidulans	ESDASCATYP	LAVAA.VTGT	TCTVPNIGSA	SLQGDARFAV		EVLRPMGCTV	
B. napus	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT	SLQGDVKFA.		EVLEKMGCKV	
A. thaliana	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT	SLQGDVKFA.		EVLEKMGCKV	
N. tabacum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTS	SLQGDVKFA.		EVLEKMGAEV	
L. esculentum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTS	SLQGDVKFA.		EVLEKMGAEV	
P. hybrida	EGDASSASYF	LAGAA.VTGG	TITVEGCGTN	SLQGDVKFA.		EVLEKMGAEV	
Z. mays	EGDASSASYF	LAGAA.ITGG	TVTVEGCGTT	SLQGDVKFA.		EVLEMMGAKV	
S. gallinarum	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIRFA.		DVLEKMGATI	
S. typhimurium	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIRFA.		DVLEKMGATI	
S. typhi	EGDASSASYF	LAAGG.IKGG	TVKVTGIGGK	SMQGDIRFA.		DVLHKGMGATI	
E. coli	EGDASSASYF	LAAA.IKGG	TVKVTGIGRN	SMQGDIRFA.		DVLEKMGATI	
K. pneumoniae	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRN	SVQGDIRFA.		DVLEKMGATV	
Y. enterocolitica	EGDASSASYF	LAAA.IKGG	TVRVTGIGKQ	SVQGDTKFA.		DVLEKMGAKI	
H. influenzae	EGDASSASYF	LAAGA.IK.G	KVKVTGIGKN	SIQGDRLFA.		DVLEKMGAKI	
P. multocida	EGDASSASYF	LAAA.IK.G	KVKVTGVGKN	SIQGDRLFA.		DVLEKMGAKI	
A. salmonicida	EGDASSASYF	LAAGA.IK.G	KVRVTGIGKH	SI.GDIHFA.		DVLERMGARI	
B. pertussis	EGDASTASYF	LALGA.IGGG	PVRVTGVGED	SIQGDVAF.		ATLAAMGADV	
Consensus	--D-S----	-----	-----	-----		-----MG---	

Figure 20G

351	PG2982	EVNLNARLAGG	EDVADLRVR.	ASKLKGVVVP	PERAPSMIDE	YPVLAIAASF	400
	LBAA	EVNLNARLAGG	EDVADLRVR.	ASKLKGVVVP	PERAPSMIDE	YPVLAIAASF	
	Agrobacterium CP4	EVINPRLAGG	EDVADLRVR.	SSTLKGVTVP	EDRAPSMIDE	YPILAVAAAF	
	B. subtilis	EIKPSADSGA	EPYGDLLIE.	TSSLKAVEIG	GDIIPRLIDE	IPIIALLATQ	
	S. aureus	QL.FNQTTGA	EPTASIRIQY	TPMLQIPITIE	GELVPKAIDE	LPVIALLCCTQ	
	S. cerevisiaeTQTATS	TTVSGPPV..	...GTLKPLK	HVDMPEMTDA	FLTACVVAAI	
	A. nidulansEQTETS	TTVTGPSD..	...GILRATS	KRGYGT.NDR	CVPRCFRTGS	
	B. napusSWTENS	VTVTGPSRDA	FGMRHLRAV.	DVNMNKMPPDV	AMTLAVVALF	
	A. thalianaSWTENS	VTVTGPPRDA	FGMRHLRAI.	DVNMNKMPPDV	AMTLAVVALF	
	N. tabacumTWTENS	VTVKGPFRNS	SGMKHLRAV.	DVNMNKMPPDV	AMTLAVVALF	
	L. esculentumTWTENS	VTVKGPFRNS	SGMKHLRAI.	DVNMNKMPPDV	AMTLAVVALF	
	P. hybridaTWTENS	VTVKGPFRSS	SGRKHLRAI.	DVNMNKMPPDV	AMTLAVVALY	
	Z. maysTWTETS	VTVTGPPREP	FGRKHLKAI.	DVNMNKMPPDV	AMTLAVVALF	
	S. gallinarumTWGDDF	I.....A	CTRGELHAI.	DMDMNHIPDA	AMTIATTALF	
	S. typhimuriumTWGDDF	I.....A	CTRGELHAI.	DMDMNHIPDA	AMTIATTALF	
	S. typhiTWGDDF	I.....A	CTRGELHAI.	DMDMNHIPDA	AMTIATTALF	
	E. coliCWGDDY	I.....S	CTRGELNAI.	DMDMNHIPDA	AMTIATAALF	
	K. pneumoniaeTWGEDY	I.....A	CTRGELNAI.	DMDMNHIPDA	AMTIATAALF	
	Y. enterocoliticaSWGDDY	I.....E	CSRGELQGI.	DMDMNHIPDA	AMTIATTALF	
	H. influenzaeTWGEDF	I.....Q	AEHAELNGI.	DMDMNHIPDA	AMTIATTALF	
	P. multocidaTWGDDF	I.....Q	VEKGNLKGI.	DMDMNHIPDA	AMTIATTALF	
	A. salmonicidaTWGDDF	I.....E	AEQGPHGV.	DMDMNHIPDV	GHDHSGQSHC	
	B. pertussisRYGPGW	IETRGRVRAE	GGR..LKAF.	DADFNLIPIA	AMTAATLALY	
	Consensus	-----	-----	-----	-----D-	-----	

Figure 20H

PG2982	401	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV	450	DCTEGEMSLT
LBAA	AEG.....	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV		DCTEGEMSLT
Agrobacterium CP4	AEG.....	ATVMNGLEEL	RVKESDRLSA	VANGLKNGV		DCDEGETSLV
B. subtilis	AEG.....	TTVIKDAEEL	KVKETNRIDT	VVSELRLKGA		EIEPTADGMK
S. aureus	AVG.....	TSTIKDAEEL	KVKETNRIDT	TADMLNLLGF		ELQPTNDGLI
S. cerevisiae	SHSDPNNSAN	TTTIEGIANQ	RVKECNRIKA	MATELAKFGV		KTTELPDGIQ
A. nidulans	HRPMEKSQTT	PPVSSGIANQ	RVKECNRIKA	MKDELAKEFGV		ICREHDDGLE
B. napus	ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA		TV.EEGSDYC
A. thaliana	ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA		TV.EEGSDYC
N. tabacum	ADG.....	PTAIRDVASW	RVKETERMIA	ICTELRKLGA		TV.VEGSDYC
L. esculentum	ADG.....	PTTIRDVASW	RVKETERMIA	ICTELRKLGA		TV.VEGSDYC
P. hybrida	ADG.....	PTAIRDVASW	RVKETERMIA	ICTELRKLGA		TV.EEGPDYC
Z. mays	ADG.....	PTAIRDVASW	RVKETERMVA	IRTELTKLGA		SV.EEGPDYC
S. gallinarum	AKG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGHDI
S. typhimurium	AKG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGHDI
S. typhi	AKG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGHDI
E. coli	AKG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGHDI
K. pneumoniae	ARG.....	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA		EV.EEGEDYI
Y. enterocolitica	ADG.....	PTVIRNIYNW	RVKETDRLSA	MATELRKVGA		EV.EEGQDYI
H. influenzae	SNG.....	ETVIRNIYNW	RVKETDRLTA	MATELRKVGA		EV.EEGEDFI
P. multocida	AEG.....	ETVIRNIYNW	RVKETDRLTA	MATELRKVGA		EV.EEGEDFI
A. salmonicida	LPR.....	VPPHSQHLQL	AVRD.DRCTP	CTHGHRRQA		GVSEEGTTFI
B. pertussis	ADG.....	PCRLRNIGSW	RVKETDRIHA	MHTELEKLGA		GV.QSGADWL
Consensus	-----	-----	-V-----R-	-----		-----

Figure 20I

PG2982	451	VRGRPDGKGL	G...GG....	TVATHLDHRI	AMSFLVMGLA	500
LBAA		VRGRPDGKGL	G...GG....	TVATHLDHRI	AMSFLVMGLAA
Agrobacterium CP4		VRGRPDGKGL	GNASGA....	AVATHLDHRI	AMSFLVMGLVA
B. subtilis		VYGKQTLKG.GA....	AVSSHGDHRI	GMMLGIASCIS
S. aureus		IHPSEFKTN.AT....	DI..LTDHRI	GMMLAVACVLT
S. cerevisiae		VHGLNSIKDL	KVPSDSSGPV	GVCTYDDHRV	AMSFSLLAGMS
A. nidulans		IDGIDR.SNL	RQPVG....	GVFCYDDHRV	AFSFSVL.SL	VNSQNERDEV
B. napus		VITP..PAKV	KPA.....	EIDTYDDHRM	AMAFSLAAC.	VTPQ.....
A. thaliana		VITP..PKKV	KTA.....	EIDTYDDHRM	AMAFSLAAC.A
N. tabacum		IITP..PEKL	NVT.....	EIDTYDDHRM	AMAFSLAAC.A
L. esculentum		IITP..PEKL	NVT.....	EIDTYDDHRM	AMAFSLAAC.A
P. hybrida		IITP..PEKL	NVT.....	DIDTYDDHRM	AMAFSLAAC.A
Z. mays		IITP..PEKL	NVT.....	AIDTYDDHRM	AMAFSLAAC.A
S. gallinarum		RITP..PAKL	QHA.....	DIGTYNDHRM	AMCFSLVAL.S
S. typhimurium		RITP..PAKL	QHA.....	DIGTYNDHRM	AMCFSLVAL.S
S. typhi		RITP..PAKL	QHA.....	DIGTYNDHRM	AMCFSLVAL.S
E. coli		RITP..PEKL	NFA.....	EIATYNDHRM	AMCFSLVAL.S
K. pneumoniae		RITP..PLTL	QFA.....	EIGTYNDHRM	AMCFSLVAL.S
Y. enterocolitica		RVVP..PAQL	IAA.....	EIGTYNDHRM	AMCFSLVAL.S
H. influenzae		RIQPLALNQF	KHA.....	NIETYNDRM	AMCFSLLIAL.S
P. multocida		RIQPLNLAQF	QHA.....	ELNI.HDHRM	AMCFALIAL.S
A. salmonicida		TRDAADPAQA	RRD.....	R..HLQRSRI	AMCFSLVAL.S
B. pertussis		EVAPPEPGGW	RDA.....	HIGTWDDHRM	AMCFLLAFF.G
Consensus		-----	-----	-----R-	-----	-----

Figure 20J

501	PG2982	EKPVTVDDSN	MIATSFPEFM	DMMPGLGAKI	ELSIL...	538
	LBAA	EKPVTVDDSN	MIATSFPEFM	DMMPGLGAKI	ELSIL...	
	Agrobacterium CP4	ENPVTVDDAT	MIATSFPEFM	DLMAGLGAKI	ELSDTKAA	
	B. subtilis	EEPIEIEHTD	AIHVSYPTEF	EHLNKLKSKS	
	S. aureus	SEPVKIKQFD	AVNVSFPGFL	PKLKLQNEG	
	S. cerevisiae	ANPVRILERH	CTGKTWPGWW	DVLH.....	
	A. nidulans	..PTLILEKE	CVGKTWPGWW	DTLRQLFKV.	
	B. napus	DVPVTIKDPG	CTRKTFFPDYF	QVLESITKH.	
	A. thaliana	DVPITINDSG	CTRKTFFPDYF	QVLERITKH.	
	N. tabacum	DVPVTIKDPG	CTRKTFFPNYF	DVLQQYSKH.	
	L. esculentum	DVPVTIKNPG	CTRKTFFPDYF	EVLQKYSKH.	
	P. hybrida	DVPVTINDPG	CTRKTFFPNYF	DVLQQYSKH.	
	Z. mays	EVPVTIRDPG	CTRKTFFPDYF	DVLSTFVKN.	
	S. gallinarum	DTPVTILDPK	CTAKTFFPDYF	EQLARMSTPA	
	S. typhimurium	DTPVTILDPK	CTAKTFFPDYF	EQLARMSTPA	
	S. typhi	DTPVTILDPK	CTAKTFFPDYF	EQLARMSTPA	
	E. coli	DTPVTILDPK	CTAKTFFPDYF	EQLARISQAA	
	K. pneumoniae	DTPVTILDPK	CTAKTFFPDYF	GQLARISTLA	
	Y. enterocolitica	DTPVTILDPK	CTAKTFFPDYF	EQLARLSQIA	
	H. influenzae	NTPVTILDPK	CTAKTFFTEFF	NEFE....KI	CLKN.....	
	P. multocida	KTSVTILDPS	CTAKTFFPTEFL	ILFTLNTREV	AYR.....	
	A. salmonicida	DIAVTINDPG	CTSKTFFPDYF	DKLASVSQAV	
	B. pertussis	PAAVRILDPG	CVSKTFFPDYF	DVYAGLLAAR	D.....	
	Consensus	-----P-----	-----P-----	-----P-----	-----P-----	

Figure 20K

ACGGGCTGTA ACGGTAGTAG GGGTCCCAG CACAAAAGCG GTGCCGGCAA GCAGAACTAA 60
TTTCCATGGG GAATAATGGT ATTTTCATGG TTTGGCCTCT GGTCTGGCAA TGGTTGCTAG 120
GCGATCGCCT GTTGAAATTA ACAAACTGTC GCCCTTCCAC TGACCATGGT AACGATGTTT 180
TTTACTTTCCT TGACTAACCG AGGAAAATTT GGCGGGGGGC AGAAATGCCA ATACAATTTA 240
GCTTGGTCTT CCCTGCCCCCT AATTGTCCCC CTCC ATG GCC TTG CTT TCC CTC 292
Met Ala Leu Leu Ser Leu
1 5
AAC AAT CAT CAA TCC CAT CAA CGC TTA ACT GTT AAT CCC CCT GCC CAA 340
Asn Asn His Gln Ser His Gln Arg Leu Thr Val Asn Pro Pro Ala Gln
10 15 20
GGG GTC GCT TTG ACT GGC CGC CTA AGG GTG CCG GGG GAT AAA TCC ATT 388
Gly Val Ala Leu Thr Gly Arg Leu Arg Val Pro Gly Asp Lys Ser Ile
25 30 35
TCC CAT CGG GCC TTG ATG TTG GGG GCG ATC GCC ACC GGG GAA ACC ATT 436
Ser His Arg Ala Leu Met Leu Gly Ala Ile Ala Thr Gly Glu Thr Ile
40 45 50
ATC GAA GGG CTA CTG TTG GGG GAA GAT CCC CGT AGT ACG GCC CAT TGC 484
Ile Glu Gly Leu Leu Leu Gly Glu Asp Pro Arg Ser Thr Ala His Cys
55 60 65 70

Figure 21A

532 TTT CGG GCC ATG GGA GCA GAA ATC AGC GAA CTA AAT TCA GAA AAA ATC
 Phe Arg Ala Met 75 Gly Ala Glu Ile Ser Glu Leu Asn Ser Glu Lys Ile 85
 580 ATC GTT CAG GGT CGG GGT CTG GGA CAG TTG CAG GAA CCC AGT ACC GTT
 Ile Val Gln Gly Arg Gly Leu Gly 95 Gln Glu Pro Ser Thr Val 100
 628 TTG GAT GCG GGG AAC TCT GGC ACC ACC ATG CGC TTA ATG TTG GGC TTG
 Leu Asp Ala Gly Asn Ser Gly Thr Thr Met Arg Leu Met Leu Gly Leu 115
 676 CTA GCC GCG CAA AAA GAT TGT TTA TTC ACC GTC ACC GGC GAT GAT TCC
 Leu Ala Gly Gln Lys Asp 120 Cys Leu Phe Thr Thr Val Thr Gly Asp Asp Ser 130
 724 CTC CGT CAC CGC CCC ATG TCC CGG GTA ATT CAA CCC TTG CAA CAA ATG
 Leu Arg His Arg Pro Met Ser Arg Val Ile Gln Pro Leu Gln Gln Met 145
 135 140
 772 GGG GCA AAA ATT TGG GCC CGG AGT AAC GGC AAG TTT GCG CCG CTG GCA
 Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly Lys Phe Ala Pro Leu Ala 160
 155 165
 820 GTC CAG GGT AGC CAA TTA AAA CCG ATC CAT TAC CAT TCC CCC ATT GCT
 Val Gln Gly Ser Gln Leu Lys Pro Ile His Tyr His Ser Pro Ile Ala 175
 170 180

Figure 21B

TCA GCC CAG GTA AAG TCC TGC CTG TTG CTA GCG GGG TTA ACC ACC GAG	868
Ser Ala Gln Val Lys Ser Cys Leu Leu Leu Ala Gly Leu Thr Thr Glu	185 190 195
GGG GAC ACC ACG GTT ACA GAA CCA GCT CTA TCC CCG GAT CAT AGC GAA	916
Gly Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu	200 205 210
CGC ATG TTG CAG GCC TTT GGA GCC AAA TTA ACC ATT GAT CCA GTA ACC	964
Arg Met Leu Gln Ala Phe Gly Ala Lys Leu Thr Ile Asp Pro Val Thr	215 220 225 230
CAT AGC GTC ACT GTC CAT GGC CCG GCC CAT TTA ACG GGG CAA CGG GTG	1012
His Ser Val Thr Val His Gly Pro Ala His Leu Thr Gly Gln Arg Val	235 240 245
GTG GTG CCA GGG GAC ATC AGC TCG GCG GCC TTT TGG TTA GTG GCG GCA	1060
Val Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala	250 255 260
TCC ATT TTG CCT GGA TCA GAA TTG TTG GTG GAA AAT GTA GGC ATT AAC	1108
Ser Ile Leu Pro Gly Ser Glu Leu Leu Val Glu Asn Val Gly Ile Asn	265 270 275
CCC ACC AGG ACA GGG GTG TTG GAA GTG TTG GCC CAG ATG GGG GCG GAC	1156
Pro Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp	280 285 290

Figure 21C

ATT ACC CCG GAG AAT GAA CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT Ile Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp 295 300 305 310	1204
CTG CGG GTT AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA Leu Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu 315 320 325	1252
ATT ATT CCC CGA CTG ATT GAT GAA ATT CCC ATT TTG GCA GTG GCG GCG Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala 330 335 340	1300
GCC TTT GCA GAG GGC ACT ACC CGC ATT GAA GAT GCC GCA GAA CTG AGG Ala Phe Ala Glu Gly Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg 345 350 355	1348
GTT AAA GAA AGC GAT CGC CTG CGC GCC ATT GCT TCG GAG TTG GGC AAA Val Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys 360 365 370	1396
ATG GGG GCC AAA GTC ACC GAA TTT GAT GAT GGC CTG GAA ATT CAA GGG Met Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly 375 380 385 390	1444
GGA AGC CCG TTA CAA GGG GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC Gly Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Leu Thr Asp His Arg 395 400 405	1492

Figure 21D

ATT GCC ATG GCG TTG GCG ATC GCC GCT TTA GGT AGT GGT GGT CAA ACA	1540
Ile Ala Met Ala Leu Ala Ile Ala Ala Ala Ser Gly Gly Gln Thr	
410	420
ATT ATT AAC CGG GCG GAA GCG GCC GCG ATT TCC TAT CCA GAA TTT TTT	1588
Ile Ile Asn Arg Ala Glu Ala Ala Ala Ile Ser Tyr Pro Glu Phe Phe	
425	435
GGC ACG CTA GGG CAA GTT GCC CAA GGA TAAAGTTAGA AAAACTCCTG	1635
Gly Thr Leu Gly Gln Val Ala Gln Gly	
440	445
GGCGGTTTGT AAATGTTTTA CCAAGGTAGT TTGGGGTAAA GGCCCCAGCA AGTGCTGCCA	1695
GGGTAATTTA TCCGCAATG ACCAATCGGC ATGGACCGTA TCGTTCAAAC TGGGTAATTC	1755
TCCCTTTAAT TCCTTAAAAG CTCGCTTAA ACTGCCCAAC GTATCTCCGT AATGGCGAGT	1815
GAGTAGAAGT AATGGGGCCA AACGGCGATC GCCACGGGAA ATTAAAGCCT GCATCACTGA	1875
CCACTTATAA CTTTCGGGA	1894

Figure 21E

```

TTTAAAAACA ATGAGTTAAA AAATTATTTT TCTGGCACAC GCGCTTTTTT TGCATTTTTT 60
CTCCCATTTT TCCGGCACAA TAACGTTGGT TTTATAAAAG GAAATG ATG ATG ACG 115
Met Met Thr
1
AAT ATA TGG CAC ACC GCG CCC GTC TCT GCG CTT TCC GGC GAA ATA ACG 163
Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr
5 10 15
ATA TGC GGC GAT AAA TCA ATG TCG CAT CGC GCC TTA TTA TTA GCA GCG 211
Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Ala Ala
20 25 30 35
TTA GCA GAA GGA CAA ACG GAA ATC CGC GCG TTT TTA GCG TGC GCG GAT 259
Leu Ala Glu Gly Gln Thr Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp
40 45 50
TGT TTG GCG ACG CCG CAA GCA TTG CGC GCA TTA GGC GTT GAT ATT CAA 307
Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln
55 60 65
AGA GAA AAA GAA ATA GTG ACG ATT CGC GGT GTG GGA TTT CTG GGT TTG 355
Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu
70 75 80

```

Figure 22A

CAG CCG CCG AAA GCA CCG TTA AAT ATG CAA AAC AGT GGC ACT AGC ATG	403
Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly Thr Ser Met	
85 90 95	
CGT TTA TTG GCA GGA ATT TTG GCA CCG CAG CGC TTT GAG AGC GTG TTA	451
Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu	
100 105 110 115	
TGC GGC GAT GAA TCA TTA GAA AAA CGT CCG ATG CAG CGC ATT ATT ACG	499
Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr	
120 125 130	
CCG CTT GTG CAA ATG GGG GCA AAA ATT GTC AGT CAC AGC AAT TTT ACG	547
Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr	
135 140 145	
GCG CCG TTA CAT ATT TCA GGA CCG CCG CTG ACC GGC ATT GAT TAC GCG	595
Ala Pro Leu Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala	
150 155 160	
TTA CCG CTT CCC AGC GCG CAA TTA AAA AGT TGC CTT ATT TTG GCA GGA	643
Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile Leu Ala Gly	
165 170 175	
TTA TTG GCT GAC GGT ACC ACC GCG CTG CAT ACT TGC GGC ATC AGT CGC	691
Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly Ile Ser Arg	
180 185 190 195	

Figure 22B

GAC CAC ACG GAA CGC ATG TTG CCG CTT TTT GGT GGC GCA CTT GAG ATC	739
Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala Leu Glu Ile	210
	205
	200
AAG AAA GAG CAA ATA ATC GTC ACC GGT GGA CAA AAA TTG CAC GGT TGC	787
Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu His Gly Cys	225
	220
	215
GTG CTT GAT ATT GTC GGC GAT TTG TCG GCG GCG GCG TTT TTT ATG GTT	835
Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Phe Phe Met Val	240
	235
	230
GCG GCT TTG ATT GCG CCG CGC GCG GAA GTC GTT ATT CGT AAT GTC GGC	883
Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Ile Arg Asn Val Gly	255
	250
	245
ATT AAT CCG ACG CCG GCG GCA ATC ATT ACT TTG TTG CAA AAA ATG GGC	931
Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln Lys Met Gly	275
	265
	260
GGA CGG ATT GAA TTG CAT CAT CAT CAG CGC TTT TGG GGC GCC GAA CCG GTG	979
Gly Arg Ile Glu Leu His His His Gln Arg Phe Trp Gly Ala Glu Pro Val	290
	285
	280
GCA GAT ATT GTT GTT TAT CAT TCA AAA TTG CGC GGC ATT ACG GTG GCG	1027
Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile Thr Val Ala	305
	300
	295

Figure 22C

CCG GAA TGG ATT GCC AAC GCG ATT GAT GAA TTG CCG ATT TTT TTT ATT	1075
Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile Phe Phe Ile	
310 315 320	
GCG GCA GCT TGC GCG GAA GGG ACG ACT TTT GTG GGC AAT TTG TCA GAA	1123
Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn Leu Ser Glu	
325 330 335	
TTG CGT GTG AAA GAA TCG GAT CGT TTA GCG GCG ATG GCG CAA AAT TTA	1171
Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala Gln Asn Leu	
340 345 350 355	
CAA ACT TTG GGC GTG GCG TGC GAC GTT GGC GCC GAT TTT ATT CAT ATA	1219
Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe Ile His Ile	
360 365 370	
TAT GGA AGA AGC GAT CCG CAA TTT TTA CCG GCG GTG AAC AGT TTT	1267
Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val Asn Ser Phe	
375 380 385	
GCG GAT CAT CCG ATT GCG ATG AGT TTG GCG GTG GCA GGT GTG CGC GCG	1315
Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly Val Arg Ala	
390 395 400	
GCA GGT GAA TTA TTG ATT GAT GAC GGC GCG GTG GCG GGT TCT ATG	1363
Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala Val Ser Met	
405 410 415	

Figure 22D

CCG CAA TTT CGC GAT TTT GCC GCC GCA ATT GGT ATG AAT GTA GGA GAA	1411
Pro Gln Phe Arg Asp Phe 425	
420	
AAA GAT GCG AAA AAT TGT CAC GAT TGATGGTCCT AGCGGTGTG GAAAAGGCAC	1465
Lys Asp Ala Lys Asn Cys His Asp	
440	
GGTGGCGCAA GCTT	1479

Figure 22E

PG2982	1MS	HSASPKPATA	RRSEALTGEI	RRSEALTGEI	RIPGDKSISH	40
LBAA	MS	HSASPKPATA	RRSEALTGEI	RRSEALTGEI	RIPGDKSISH	
Agrobacterium CP4	MS	HGASSRPATA	RKSSGLSGTV	RKSSGLSGTV	RIPGDKSISH	
Synechocystis sp. PCC6803		MALLSLNNHQ	SHORLTVNPP	AQGVALTGRL	AQGVALTGRL	RVPGDKSISH	
B. subtilis	MKR	DKVQTLHGEI	DKVQTLHGEI	HIPGDKSISH	
D. nodosus	MMTNIWHT	APVSALSGEI	APVSALSGEI	TICGDKSMTH	
S. aureus	MVNEQII	DISGPLKGEI	DISGPLKGEI	EVPGDKSMTH	
Consensus		-----	-----	-----L-G--	-----L-G--	-I-GDKS--H	
	41						80
PG2982		RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	GEDVINTGRA	MQAMGAKI.R	
LBAA		RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	GEDVINTGRA	MQAMGAKI.R	
Agrobacterium CP4		RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	GEDVINTGRA	MQAMGAKI.R	
Synechocystis sp. PCC6803		RALMLGAIAT	GETIIEGLLL	GEDPRSTAH	GEDPRSTAH	FRAMGAEISE	
B. subtilis		RSVMFGALAA	GTTTVKNFLP	GADCLSTIDC	GADCLSTIDC	FRKMGVHI.E	
D. nodosus		RALLLAALAE	GQTEIRGFLL	CADCLATRQA	CADCLATRQA	LRLGVDI.Q	
S. aureus		RAIMLASLAE	GVSTIYKPLL	GEDCRRTMDI	GEDCRRTMDI	FRHLGVEI.K	
Consensus		R--MF---A-	G---I---L-	--D---T---	--D---T---	---MG---I--	
	81						120
PG2982		KEGDVWIING	VNGCCLLQPE	AALDFGNAGT	AALDFGNAGT	GARLTMGLVG	
LBAA		KEGDVWIING	VNGCCLLQPE	AALDFGNAGT	AALDFGNAGT	GARLTMGLVG	
Agrobacterium CP4		KEGDTWIIDG	VNGGGLLAPE	APLDFGNAAT	APLDFGNAAT	GCRLTMGLVG	
Synechocystis sp. PCC6803		LNSEKIIVQG	RGLGQLQEPS	TVLDAGNSGT	TVLDAGNSGT	TMRMLGLLLA	
B. subtilis		QSSSDVVIHG	KGIDALKEPE	SLLDVGNST	SLLDVGNST	TIRMLGLILA	
D. nodosus		REKEIVTIRG	VGFLGLQPPK	APLNMQNSGT	APLNMQNSGT	SMRLLAGILA	
S. aureus		EDDEKLVVTS	PGYQ.VNTPH	QVLYTGNSGT	QVLYTGNSGT	TTRLLAGLLS	
Consensus		-----I--	-G-----P-	--L---N--T	--L---N--T	--RL--G---	

Figure 23A

PG2982	121	TY.DMKTSFI	GDASLSKRPM	GRVLNPLREM	GVQVEAADGD	160
LBAA		TY.DMKTSFI	GDASLSKRPM	GRVLNPLREM	GVQVEAADGD	
Agrobacterium CP4		VY.DFDSTFI	GDASLTKRPM	GRVLNPLREM	GVQVKSEDDG	
Synechocystis sp. PCC6803		GQKDCFLT	VTGDDSLRHRPM	SRVIQPLQQM	GAKIWARNSG	
B. subtilis		G.RPFYSAVA	GDESIKRPM	KRVTEPLKKM	GAKIDGRAGG	
D. nodosus		AQR.FESVLC	GDESLEKRPM	QRIITPLVQM	GAKIVSHSNF	
S. aureus		GLGN.ESVLS	GDVSIKRP	MDRVLRLPLKLM	DANIEGIEDN	
Consensus		-----	GD-S---RPM	-RV--PL--M	---I-----	
PG2982	161	RMPLTLIGPK	TANPITYRVP	MASQVKSASV	LLAGLNTPGV	200
LBAA		RMPLTLIGPK	TANPITYRVP	MASQVKSASV	LLAGLNTPGV	
Agrobacterium CP4		RLPVTLRGPK	TPTPITYRVP	MASQVKSASV	LLAGLNTPGI	
Synechocystis sp. PCC6803		KFAPLAVQGS	QLKPIHYHSP	IASAQVKSCL	LLAGLTTEGD	
B. subtilis		EFTPLSVSGA	SLKGIDYVSP	VASQIKSASV	LLAGLQAEET	
D. nodosus		T.APLHISGR	PLTGIDYALP	LPSAQLKSCL	ILAGLLADGT	
S. aureus		.YTPLIIKPS	VIKGINYQME	VASQVKSASV	LFASLFSKEP	
Consensus		-----	----I-Y---	--SAO-KS--	-LA-L-----	
PG2982	201	TTVIEPVMTR	DHTEKMLQGFGADLT	VETDKDGVRRH	240
LBAA		TTVIEPVMTR	DHTEKMLQGFGADLT	VETDKDGVRRH	
Agrobacterium CP4		TTVIEPIMTR	DHTEKMLQGFGANLT	VETDADGVRT	
Synechocystis sp. PCC6803		TTVTEPALSR	DHSERMLQAFGAKLT	IDPVTHSV..	
B. subtilis		TTVTEPHKSR	DHTEKMLQAFGVKLS	EDQT...SV..	
D. nodosus		TRLHTCGISR	DHTEKMLPLFGGALE	IKK...EQI..	
S. aureus		TIIEKELDVSR	NHTETMFKHF	NIPIEAEGLS	INTTPEAIRY	
Consensus		T-----R	-H-E-ML--F	-----L-	-----V--	

Figure 23B

PG2982	241	IRITGQGLV	GQTIDVPGDP	SSTAFPLVAA	LLVEGSDVTI	280
LBAA		IRITGQGLV	GQTIDVPGDP	SSTAFPLVAA	LLVEGSDVTI	
Agrobacterium CP4		IRLEGRGKLT	GQVIDVPGDP	SSTAFPLVAA	LLVPGSDVTI	
Synechocystis sp. PCC6803		.TVHGPahlT	GQRVVVPGDI	SSAAFWLVA	SILPGSELLV	
B. subtilis		.SIAGGQKLT	AADIFVPGDI	SSAAFFLAAG	AMVPNSRIVL	
D. nodosus		.IVTGGQKLH	GCVLDIVGDL	SAAAFMVA	LIAPRAEVVI	
S. aureus		IKPAD.....	...FHVPGDI	SSAAFFIVAA	LITPGSDVTI	
Consensus		-----	-----V-GD-	S--AF-----	-----	
	281	RNVLMNPTRT	GLILTLQEMG	ADIEVLNARL	AGGEDVADLR	320
PG2982		RNVLMNPTRT	GLILTLQEMG	ADIEVLNARL	AGGEDVADLR	
LBAA		RNVLMNPTRT	GLILTLQEMG	ADIEVINPRL	AGGEDVADLR	
Agrobacterium CP4		ENVGINPTRT	GVLEVLQMG	ADITPENERL	VTGEPVADLR	
Synechocystis sp. PCC6803		KNVGLNPTRT	GIIDVLQNMG	AKLEIKPSAD	SGAEPYGDLI	
B. subtilis		RNVGINPTRA	AIITLLQKMG	GRIELHHQRF	WGAEPVADIV	
D. nodosus		HNVGINQTRS	GIIDIVEKMG	GNIQLFNQT.	TGAEPTASIR	
S. aureus		-NV--N-TR-	-----MG	-----	---E-----	
Consensus		321				360
PG2982		VR.ASKLKG	VVPPERAPSM	IDEYPVLAIA	ASFAEGETVM	
LBAA		VR.ASKLKG	VVPPERAPSM	IDEYPVLAIA	ASFAEGETVM	
Agrobacterium CP4		VR.SSTLKG	TVPEDRAPSM	IDEYPILAVA	AAFAEGATVM	
Synechocystis sp. PCC6803		VR.ASHLQGC	TFGGEIIPRL	IDEIPILAVA	AAFAEGTTRI	
B. subtilis		IE.TSSLKAV	EIGGDIIPRL	IDEIPIIAL	ATQAEGTTVI	
D. nodosus		VY.HSKLRGI	TVAPEWIANA	IDELPIFFIA	AACAEGTTFV	
S. aureus		IQYTPMLQPI	TIEGELVPKA	IDELPVIALL	CTQAVGTSTI	
Consensus		V-----L---	-----E-----	IDE-PI----	---A-G-----	

Figure 23C

361	PG2982	DGLDELRVKE	SDRLAAVARG	LEANGVDCTE	GEMSLTVRGR	400
	LBAA	DGLDELRVKE	SDRLAAVARG	LEANGVDCTE	GEMSLTVRGR	
	Agrobacterium CP4	NGLEELRVKE	SDRLSAVANG	LKLVGVDCDE	GETSLVVGR	
	Synechocystis sp. PCC6803	EDAAELRVKE	SDRLAAIASE	LKMGAKVTE	FDDGLEIQGG	
	B. subtilis	KDAAELRVKE	TNRIDTVVSE	LRKLGAIEP	TADGMKVYK	
	D. nodosus	GNLSELRVKE	SDRLAAMAQN	LQTLGVACDV	GADFIHIYGR	
	S. aureus	KDAEELRVKE	TNRIDTTADM	LNLLGFELQP	TNDGLIIHPS	
	Consensus	----EL-VKE	--R-----	L---G-----	-----V---	
401	PG2982	PDGKGLG...	GGTVATHLDH	RIAMSFVLMG	LAAEKPVTVD	440
	LBAA	PDGKGLG...	GGTVATHLDH	RIAMSFVLMG	LAAEKPVTVD	
	Agrobacterium CP4	PDGKGLGNAS	GAAVATHLDH	RIAMSFVLMG	LVSENPVTVD	
	Synechocystis sp. PCC6803	SPLQ.....	GAEVDSLTDH	RIAMALAIAA	LGSGGQTIIN	
	B. subtilis	QTLK.G....	GAAVSSHGDH	RIGMMLGIAS	CITEEPIEIE	
	D. nodosus	SDRQFL....	PARVNSFGDH	RIAMSLAVAG	VRAAGELLID	
	S. aureus	E.....FK	TNATDILTTH	RIGMMLAVAC	VLSSEPVKIK	
	Consensus	-----	-----DH	RI-M-L-V--	-----I-	
441	PG2982	DSNMIATSFP	EFMDMMPGLG	AKIELSIL..	...	473
	LBAA	DSNMIATSFP	EFMDMMPGLG	AKIELSIL..	...	
	Agrobacterium CP4	DATMIATSFP	EFMDLMAGLG	AKIELSDTKA	A..	
	Synechocystis sp. PCC6803	RAEAAAISYP	EFFGTLGQVA	QG*.....	...	
	B. subtilis	HTDAIHVSYP	TFEHLNKLK	KKS.....	...	
	D. nodosus	DGAVAAVSMP	QFRDFAAAIG	MNVGEKDAKN	CHD	
	S. aureus	QFDVNVVSFP	GFLPKLLQ	NEG.....	...	
	Consensus	-----S-P	-F-----	-----	---	

Figure 23D

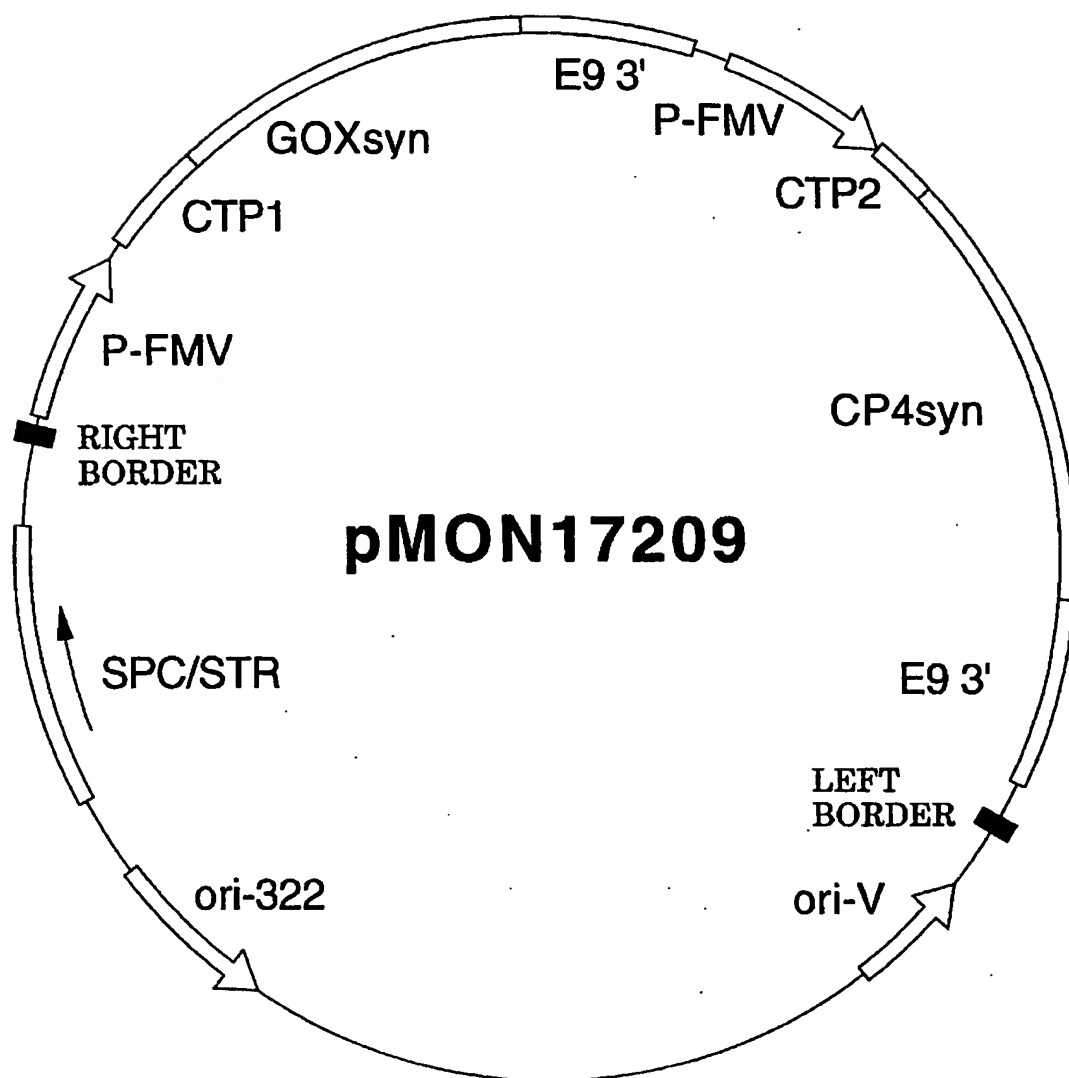


Figure 24

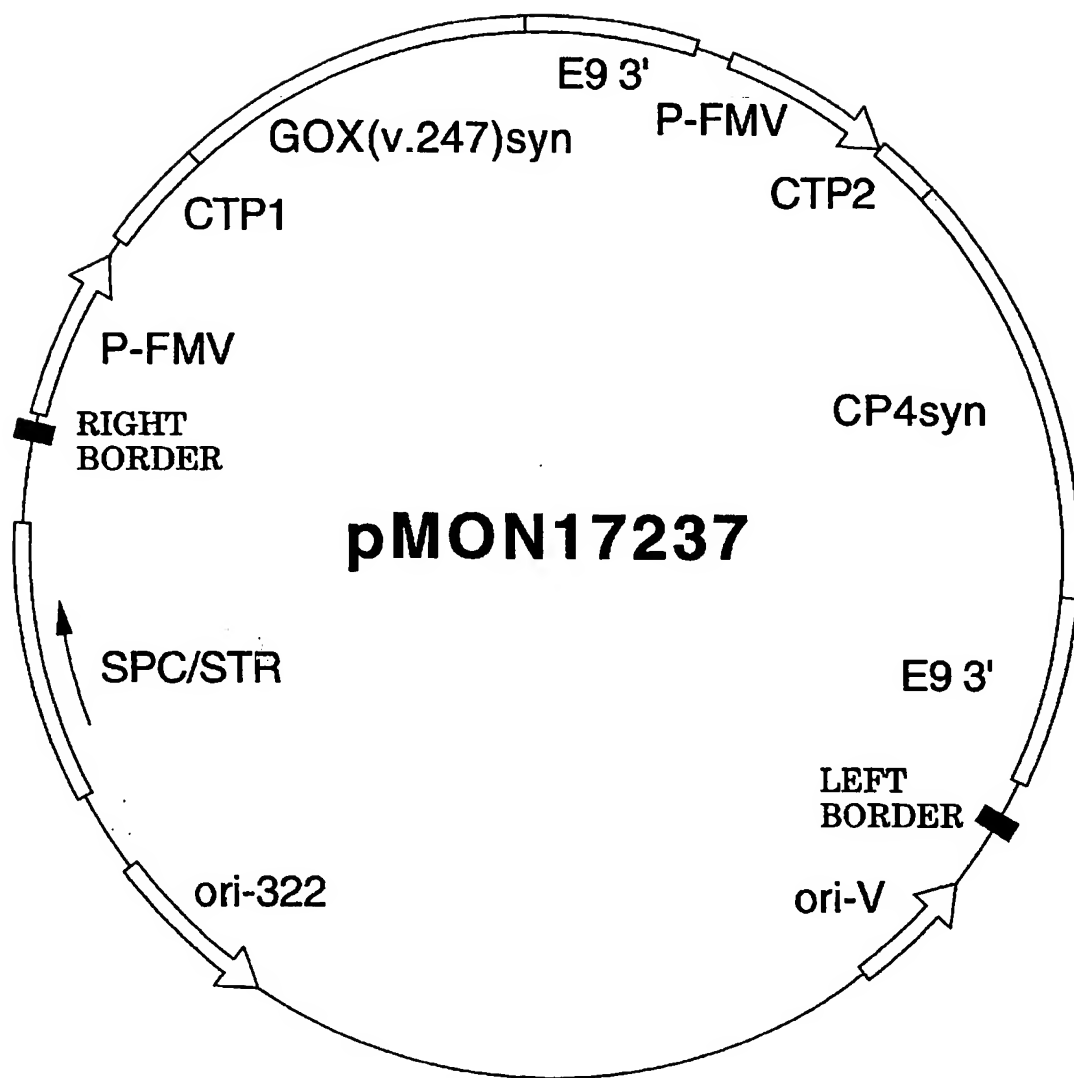


Figure 25